

XX Clancy RL, Cripps AM, Dunkley M, Kyd J;
 XX WPI; 1998-427879/36.
 XX
 XX Protein antigen from *Pseudomonas aeruginosa* and its antigenic
 XX fragments - useful diagnostically to detect specific antibodies,
 XX particularly in patients with cystic fibrosis, and as vaccines
 XX
 XX Claim 3; Page 2; 23pp; English.
 XX
 XX This peptide is the N-terminal fragment of a novel *Pseudomonas aeruginosa*
 XX protein antigen, Pa60. This fragment could be used for diagnostic
 XX detection of *P. aeruginosa* by forming complexes with specific antibodies,
 XX particularly in patients with cystic fibrosis (by analysis of mucus, e.g.
 XX in saliva), or in vaccines or immunogenic compositions to treat or
 XX prevent infection by *P. aeruginosa*.
 XX
 XX Sequence 19 AA:
 XX
 XX Query Match 93.8%; Score 76; DB 19; Length 19;
 XX Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 XX ||||||||||||||||
 XX 2 EEKTPLTAAAXAPVYXNA 19
 XX
 XX
 XX RESULT 2
 XX AAB69062
 XX ID AAB69062 standard; peptide: 19 AA.
 XX AC AAB69062;
 XX
 XX 18-APR-2001 (first entry)
 XX
 XX *Pseudomonas aeruginosa* protein N-terminal peptide.
 XX
 XX *Pseudomonas aeruginosa*; chitinase; groEL; chiA; antigen; vaccine;
 XX diagnosis; detection; infection; immune response.
 XX
 XX *Pseudomonas aeruginosa*.
 XX
 XX OS
 XX
 XX Key Location/Qualifiers
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 XX FT Misc-difference 12 /note= "unspecified"
 XX FT Misc-difference 17 /note= "unspecified"
 XX Misc-difference 17 /note= "unspecified"
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 XX WO200102577-A1.
 XX
 XX 11-JAN-2001.
 XX
 XX 03-JUL-2000; 2000WO-GB02554.
 XX
 XX 01-JUL-1999; 99GB-0015419.
 XX
 XX (PROV-) PROVALIS UK LTD.
 XX
 XX Smith CJ, Thompson SE, Smith MW, Peek K, Sizer PJH, Wilkinson MC;
 XX WPI; 2001-080988/09.
 XX
 XX Antigenic *Pseudomonas aeruginosa* proteins, useful in the detection
 XX and/or diagnosis of *P. aeruginosa* infections and for producing vaccines
 XX against *P. aeruginosa*.
 XX
 XX Disclosure; Page 2; 129pp; English.
 XX
 XX The present invention describes antigenic *Pseudomonas aeruginosa*

CC proteins (P₆₀). The *P. aeruginosa* proteins have antibacterial activity
 CC and can be used in vaccines and as antagonists. The proteins or their
 CC fragments, or antibodies are useful in the detection and/or diagnosis
 CC of *P. aeruginosa*. They are also useful for producing a vaccine and
 CC inducing an immune response against *P. aeruginosa* infection. An agent
 CC capable of antagonising, inhibiting or otherwise interfering with the
 CC function or expression of P1 are useful in the manufacture of a
 CC medicament for the treatment or prophylaxis of *P. aeruginosa* infections.
 CC The present sequence represents a probable *P. aeruginosa* protein
 CC N-terminal peptide sequence from the present invention.
 XX
 XX Sequence 19 AA:
 XX
 XX Query Match 93.8%; Score 76; DB 22; Length 19;
 XX Best Local Similarity 100.0%; Pred. No. 3.1e-06;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 XX AC AAG30091;
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 XX 17-OCT-2000 (first entry)
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 XX Protein identification; signal transduction pathway; metabolic pathway;
 XX hybridisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.
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 XX Arabidopsis thaliana.
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 XX 25-FEB-2000; 2000EP-0301439.
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Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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XX AAG30090;
DE 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 35911.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35911.
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX EPI033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
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XX 05-MAR-1999; 99US-0123180.
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XX 23-MAR-1999; 99US-0125788.
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| PR | 29-OCT-1999: | 99US-0162142. |

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| DB | 73 | EKAEMTTAMOSPV 87 |

RESULT 5
ABB52865
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AC ABB52865;
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DT 11-FEB-2002 (first entry)
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XX
XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
KW systemic infection; non-diarrhoeal infection; septicaemia;
KW pyelonephritis; antibiotic resistance.
OS Escherichia coli.
XX
PN WO200166572-A2.
XX
PD 13-SEP-2001.
XX
PE 12-MAR-2001; 2001MO-EP03445.
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XX 10-MAR-2000; 2000FR-0003145.
PR 02-FEB-2001; 2001FR-0001449.
XX
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Bingen E, Bonaccorsi S, Clermont O, Nassif X, Tinsley C;
XX WPI; 2001-550253/61.
DR
PT A library of DNA fragments of Escherichia coli strains for the
PT phylogenetic determination of a given strain comprises polynucleotides of
PT nature B2/D+ A- .
XX
XX
PS Example 6; Fig 6; 646pp; English.
XX
XX The invention relates to a library of DNA fragments of Escherichia coli
CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89333)
CC and encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of nature
CC B2/D+A-. The polynucleotides have potential antiinflammatory,
CC antibacterial and immunosuppressive activity as part of pharmaceutical
CC compositions used to treat, palliate or prevent extra-intestinal E. coli
CC infections. The polypeptides are useful for determining the phylogenic
CC group of a given E. coli strain. These polypeptides can detect and treat
CC an undesired development of E. coli strain. These polypeptides can detect and treat
CC infection that include systemic and non-diarrhoeal infections such as
CC septicaemia, pyelonephritis and meningitis this is particularly
CC advantageous as bacterial resistance is increasing with the more
CC frequent use of broad spectrum antibiotics.
XX
XX
SQ Sequence 306 AA:

| | | | | |
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| Query Match | 54.3% | Score 44: | DB 22: | Length 306: |
| Best Local Similarity | 47.1% | Pred. No. 18: | | |
| Matches 8: | Conservative 3: | Mismatches 6: | Indels 0: | Gaps 0: |

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| QY | 3 | EKTPLTAAAPVXNA 19 |
| DB | 84 | EKVPTSSGVAPFPVNA 100 |

| | | |
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| ID | AA067588 | standard; Protein; 306 AA. |
| AC | AA067588; | |
| XX | | |
| DT | 29-MAY-2001 | (first entry) |
| XX | | |
| DE | Amino acid sequence of a deoxyribokinase enzyme. | |
| XX | | |
| KW | Deoxyribonucleoside; deoxyribose 1-phosphate; thymidine phosphorylase; | |
| KW | purine nucleoside phosphorylase; phosphopentose mutase; | |
| KW | phosphopentose aldolase; fructose 1,6-diphosphate aldolase; | |
| KW | deoxyribokinase; nucleoside 2-deoxyribosyltransferase. | |
| XX | | |
| OS | Salmomella typhi. | |
| XX | | |
| PN | W0200114566-A2. | |
| XX | | |
| PD | 01-MAR-2001. | |
| XX | | |
| 18-AUG-2000; | 2000WO-EP08088. | |
| 20-AUG-1999; | 99EP-0116425. | |
| XX | | |
| PA | (HOFF) ROCHE DIAGNOSTICS GMBH. | |
| PA | (INSP) INST PASTEUR. | |
| PA | (PHAR-) PHARMA-WALDHOFF GMBH & CO KG. | |
| XX | | |
| PI | Tischer W, Ihlenfeldt H, Barzu O, Sakamoto H, Pistotnik E; | |
| PI | Marliere P, Pochet S; | |
| XX | | |
| DR | WPI: 2001-235026/24. | |
| DR | N-PSDB: AAF55444. | |
| XX | | |
| PT | In vitro enzymatic synthesis of deoxyribonucleosides comprises reacting | |
| PT | deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside | |
| PT | and an inorganic phosphate | |
| XX | | |
| XX | Disclosure: Page 59-61; 73pp; English. | |
| XX | | |
| CC | The present sequence represents a deoxyribokinase enzyme. This enzyme | |
| CC | is involved in the biosynthesis of deoxyribonucleosides, and is | |
| CC | used in the method of the invention. The specification describes a | |
| CC | method for the in vitro enzymatic synthesis of deoxyribonucleosides. | |
| CC | The method comprises reacting deoxyribose 1-phosphate and a nucleobase | |
| CC | to form a deoxyribonucleoside and an inorganic phosphate. | |
| CC | Enzymes which | |
| CC | may be used in the method of the invention include thymidine | |
| CC | phosphorylase, purine nucleoside phosphorylase, phosphopentose mutase, | |
| CC | phosphopentose aldolase, fructose 1,6-diphosphate aldolase, | |
| CC | deoxyribokinase, and nucleoside 2-deoxyribosyltransferase. | |
| XX | | |
| XX | Sequence | 306 AA: |
| XX | | |
| XX | Query Match | 54.3%; Score 44; DB 22; Length 306; |
| XX | Best Local Similarity | 47.1%; Pred. No. 18; |
| XX | Matches | 8; Conservative |
| XX | | 3; Mismatches |
| XX | | 6; Indels |
| XX | | 0; Gaps |
| XX | 3 EKTPLTFAAXAPVYXNA 19 | |
| XX | ::: : | |
| DB | 84 EKVPTCTSSGVAPLEFVNA 100 | |
| XX | | |
| XX | RESULT 7 | |
| XX | AAG30089 | |
| XX | ID AAG30089 standard; Protein; 427 AA. | |
| XX | AC AAG30089; | |
| XX | | |
| XX | 17-OCT-2000 (first entry) | |
| XX | | |
| DE | Arabidopsis thaliana protein fragment SEQ ID NO: 35910. | |
| XX | | |
| XX | Protein identification; signal transduction pathway; metabolic pathway; | |
| XX | hybridisation assay; genetic mapping; gene expression control; promoter; | |

| | | |
|----|---------------------------------|--|
| KW | termination sequence. | |
| XX | <i>Arabicidopsis thaliana</i> . | |
| OS | EpI033405-A2. | |
| PM | | |
| XX | 06-SEP-2000. | |
| PD | | |
| XX | | |
| XX | | |
| PE | 25-FEB-2000; 2000EP-0301439. | |
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| PR | 30-APR-1999; 9905-0132048. | |
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| PR | 14-MAY-1999; 9905-0134321. | |
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| PR | 27-MAY-1999; 9905-0136391. | |
| PR | 28-MAY-1999; 9905-0136782. | |
| PR | 01-JUN-1999; 9905-0137222. | |
| PR | 03-JUN-1999; 9905-0137526. | |
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| PR | 07-JUN-1999; 9905-0137740. | |
| PR | 08-JUN-1999; 9905-0138094. | |
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| PR | 14-JUN-1999; 9905-0139319. | |
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 PR 99US-0152353.

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Query Match 54.3%; Score 44; DB 21; Length 427;
 Best Local Similarity 60.0%; Pred. No. 27;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 EKKTPLTAAAPV 16
 Db 208 EKKAMTTAMSPV 222
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 AAG43604
 ID AAG43604 standard; Protein; 172 AA.
 AC AAG43604;
 XX
 XX 18-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 54519.
 XX
 XX Protein identification: signal transduction pathway; metabolic pathway;
 KM hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.
 XX Arabidopsis thaliana.
 OS
 XX
 XX EP1033405-A2.
 PN
 XX
 PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.
 PE
 XX
 PR 05-FEB-1999; 99US-0121825.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 51.9%; Score 42; DB 21; Length 172;
 Best Local Similarity 50.0%; Pred. No. 21;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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 Db 131 EERTPEKKTGVPVAKA 148

RESULT 9
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 ID AAC43603 standard; Protein; 215 AA.

XX AAC43603;
 XX 18-OCT-2000 (first entry)
 DT Arabidopsis thaliana protein fragment SEQ ID NO: 54518.
 DE
 XX
 XX Protein identification: signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 OS Arabidopsis thaliana.
 XX
 XX EPI033405-A2.
 PM
 XX 06-SEP-2000.
 PD
 XX 25-FEB-2000; 2000EP-0301439.
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 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-012180.
 PR 09-MAR-1999; 99US-0123548.
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AC AAG43602;

DT 18-OCT-2000 (first entry)

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| AA | DE | Arabidopsis thaliana protein fragment | SEQ ID NO: 54517. |

KW protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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PR 09-MAR-1999; 99US-0123548.

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 DB 291 EEKTPVEKKTGVPYKKA 308

RESULT 11

ABB66926
 ID ABB66926 standard; Protein; 1012 AA.

AC ABB66926;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 27570.

XX Drosophila: developmental biology; cell signalling; insecticide;

KW pharmaceutical.

OS Drosophila melanogaster.

XX WO200171042-A2.

27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL11029.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

XX interactions -

PS Disclosure; SEQ ID NO 27570; 21bp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins

CC (AB57737-AB872072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1012 AA;

QY 2 EEKPLTTAAAXAPV 16
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 DB 695 EEVTPYNTAPHSPIV 709

Query Match 50.6%; Score 41; DB 22; Length 1012;
 Best Local Similarity 53.3%; Pred. No. 2; 3e-02;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

DE Listeria monocytogenes protein #1186.

XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;

KW vitamin B12; bacterial infection; disease.

OS Listeria monocytogenes.

XX WO200177335-A2.

XX 18-OCT-2001.

PF 11-APR-2001; 2001WO-FR01118.

PR 11-APR-2000; 2000FR-0004629.

PA (INSP) INST PASTEUR.

XX Buchrieser C, Frangeul L, Couve E, Rusnlok C, Faehl H, Dehoux P;

PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;

PI Daniels J, Goebel W, Krefit J, Kuhn M, Ng E, Vazquez-Boland JA;

PI Domínguez-Bernal G, Garrido-García P, Rierrez-Martínez A, Amend A;

PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;

PI Perez-Diaz J, Baquero F, García Del Portillo F, Gomez-Lopez N;

PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;

PI Rose M, Voss H;

XX WPI; 2002-010914/01.

DR Genomic sequence for Listeria monocytogenes, useful e.g. for treatment

PT and prevention of Listeria and related bacterial infections, and

PT related polypeptides -

XX Claim 6; SEQ ID NO 1187; 192bp; French.

XX The present invention relates to the genome sequence of Listeria

CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of

CC it are useful for selecting probes and primers for detecting genes in L.

CC monocytogenes and related organisms. The present sequence is a protein

CC polymorphisms and other genomes. The present invention. Proteins

CC encoded by the genome sequence of the present invention. Proteins

CC expressed from the genome sequence are useful for raising specific

CC antibodies, identification of L. monocytogenes and related organisms, and

CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin

CC B12. The genome sequence and proteins encoded by it are also useful for

CC selecting compounds that regulate gene expression and cell replication

CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccine compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
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Best Local Similarity 57.1%; Pred. No. 73;
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QY 3 EKTPLTTAAAXAPV 16
DB 158 EETELTNVAVYAPVI 171

RESULT 13

ID AU36108 standard; Protein: 445 AA.

AC AU36108;

DT 14-FEB-2002 (first entry)

DE Klebsiella pneumoniae cellular proliferation protein #96.

KW Antisense; prokaryotic cellular proliferation protein;

OS antibiotic; antibacterial; drug design.

XX Klebsiella pneumoniae.

PN WO200170955-A2.

PD 27-SEP-2001.

PF 21-MAR-2001; 2001WO-US09180.

PR 21-MAR-2000; 2000US-191078P.

PR 23-MAY-2000; 2000US-206848P.

PR 26-MAY-2000; 2000US-207727P.

PR 23-OCT-2000; 2000US-242578P.

PR 23-NOV-2000; 2000US-253625P.

PR 22-DEC-2000; 2000US-257931P.

PR 16-FEB-2001; 2001US-269308P.

XX (ELIT-) ELITRA PHARM INC.

PI Haselbeck R, Ohlson KL, Zyckind JW, Wall D, Trawick JD, Carr GJ;

PI Yamamoto RT, Xu HH;

XX WPI: 2001-611495/70.

DR N-PSDB; AAS53967.

XX

CC

CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
CC
SQ Sequence 445 AA;

Query Match 49.4%; Score 40; DB 22; Length 445;
Best Local Similarity 57.1%; Pred. No. 13+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKTPLTTAAAXAPV 15
DB 382 EKTPLTTADMAAI 395

RESULT 14

ID AAR51691 standard; Protein: 498 AA.

AC AAR51691;

DT 07-NOV-1994 (first entry)

DE HIV-type virus WVP5180/91 gag protein (cloned).

KW Human immunodeficiency virus; HIV; antigen; detection; diagnosis;

OS retrovirus; vaccine; lymphocyte; reverse transcriptase.

XX HIV-type virus WVP-5180/91 (ECACC V92092318).

PN EP591914-A.

PD 13-APR-1994.

PF 05-OCT-1993; 93EP-0116058.

PR 06-OCT-1992; 92DE-4233646.

PR 22-OCT-1992; 92DE-4235718.

PR 30-DEC-1992; 92DE-4244541.

PR 01-JUN-1993; 93DE-4318186.

PA (BEHM) BEHRINGWERKE AG.

PI Bruun VA, Eberle J, Gurtler LG, Hauser H-P, Knapp S;

PI WPI: 1994-120077/15.

DR N-PSDB; AAO58974.

XX

CC

CC

CC

CC

CC

CC The virus consists of RNA in a peg-shaped core made of p24 subunits
CC surrounded by an outer core of p17 and then a glycoprotein envelope
CC which, apart from host-cell derived lipids, comprises gp41 and
CC envelope protein gp120 (which can bind to the CD4 receptor).
CC Related viruses have at least 75% homology over the entire
CC genome with max. differences for the various regions LTR and NEF

Query Match 49.4%; Score 40; DB 22; Length 445;
Best Local Similarity 57.1%; Pred. No. 13+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKTPLTTAAAXAPV 15
DB 382 EKTPLTTADMAAI 395

RESULT 14

ID AAR51691 standard; Protein: 498 AA.

AC AAR51691;

DT 07-NOV-1994 (first entry)

DE HIV-type virus WVP5180/91 gag protein (cloned).

KW Human immunodeficiency virus; HIV; antigen; detection; diagnosis;

OS retrovirus; vaccine; lymphocyte; reverse transcriptase.

XX HIV-type virus WVP-5180/91 (ECACC V92092318).

PN EP591914-A.

PD 13-APR-1994.

PF 05-OCT-1993; 93EP-0116058.

PR 06-OCT-1992; 92DE-4233646.

PR 22-OCT-1992; 92DE-4235718.

PR 30-DEC-1992; 92DE-4244541.

PR 01-JUN-1993; 93DE-4318186.

PA (BEHM) BEHRINGWERKE AG.

PI Bruun VA, Eberle J, Gurtler LG, Hauser H-P, Knapp S;

PI WPI: 1994-120077/15.

DR N-PSDB; AAO58974.

XX

CC

CC

CC

CC

CC

CC 108, POL 128, GAG 148, VIF 158 and ENV 228.

Sequence 498 AA;

| Query Match | Score | DB | Length |
|-------------|-------|-----|--------|
| 49.48; | 40; | 15; | 498; |

| | | | | | | | | | |
|------------|------------|--------------|----------|------------|----|--------|----|------|----|
| Best Local | Similarity | 44.48; | Pred.No. | 1.3e+02; | | | | | |
| Matches | 8; | Conservative | 3; | Mismatches | 7; | Indels | 0; | Gaps | 0; |

Matches 8; Conservative

2 EЕКТРЛТАХАРVXNA 19

Db 119 EETSPRQTSQNPVTNA 136

RESULT 15

AAW93076 standard; Protein; 498 AA
ID AAW93076

XX
XX
20103076-

19-MAY-1999 (first entry)

HIV isolate 5180 gag protein.

XX HIV-type retrovirus; MWP-5180/91; ECACC V 92092318; antigen; assay kit;
KW

KW detection; antibody; immune deficiency; vaccine.

OS Human immunodeficiency virus

PN EP890642-A2.

PD 13-JAN-1999

PF 05-OCT-1993; 93EP-0116058.

PR 01-JUN-1993; 93DEF-4318186

PR 22-OCT-1992; 92DE-4235718

| | | |
|----|-------------|---|
| XX | 20 DEC 1961 | 1 |
| XX | | |

XX
XX
XX

PI Brunn AV, Ederle J, Guerrieri ES
XY

DR WPI; 1999-072878/07.

PT New HIV-type retrovirus antigen - used for

PT deficiency and to prepare vaccines

Example 11; Fig 7; 39pp; German -

This invention describes the isolation of a novel HIV-type retrovirus called MWP-5180/91 (ECACC V 92092318). Antigens produced from this product can be used in an assay kit for detecting antibodies against viruses that cause immune deficiency, preferably where the assay is a Western blot, ELISA or fluorescence immunoassay. MWP-5180/91, cDNA and/or antigen can be used for detecting retroviruses that cause immune deficiency and to prepare vaccines. This sequence represents an HIV MWP 5180 gag protein.

SQ Sequence 498 AA;

| | | | | |
|-------------|--------|------------|--------|-------------|
| Query match | 49.48; | Score 40; | DB 20; | Length 498; |
| | 44.48; | Prod NO. 1 | 5e+02; | |

| | | | | | | | | | |
|---------|----|--------------|----|------------|----|--------|----|------|----|
| | 8; | Conservative | 3; | Mismatches | 7; | Indels | 0; | Gaps | 0; |
| Matches | | | | | | | | | |

2 ЕКРПЛТААХАРВХНА 19
QY

Db 119 EETSPROTSONYPIVTNA 136

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Search completed: March 14, 2003, 09:11:28
Job time : 38 secs
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GenCore version 5.1.4.p5.4578
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OK protein - protein search, using sw model

Run on: March 14, 2003, 09:10:49 ; Search time 14 seconds
(without alignments)
39.931 Million cell updates/sec

Title: US-09-359-426C-2

Sequence: 1 XEERTPLTTAAKAPVXNA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_Aa.*
1: /cgn2-6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2-6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2-6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2-6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2-6/ptodata/2/1aa/PTCUTS_COMB.pep.*
6: /cgn2-6/ptodata/2/1aa/Backfilest1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|---------------------------|-------------------|
| 1 | 41 | 50.6 | 788 1 US-08-194-338-12 | Sequence 12, Appl |
| 2 | 40 | 49.4 | 498 1 US-08-470-202-59 | Sequence 59, Appl |
| 3 | 40 | 49.4 | 498 1 US-08-471-770-59 | Sequence 59, Appl |
| 4 | 40 | 49.4 | 498 2 US-08-468-059-59 | Sequence 59, Appl |
| 5 | 40 | 49.4 | 498 4 US-09-109-916-59 | Sequence 59, Appl |
| 6 | 37 | 45.7 | 456 1 US-08-624-125-20 | Sequence 20, Appl |
| 7 | 37 | 45.7 | 463 2 US-08-679-635A-4 | Sequence 4, Appl |
| 8 | 37 | 45.7 | 463 4 US-09-419-163-4 | Sequence 4, Appl |
| 9 | 36 | 44.4 | 19 3 US-08-943-173-8 | Sequence 8, Appl |
| 10 | 36 | 44.4 | 38 3 US-08-943-173-16 | Sequence 16, Appl |
| 11 | 36 | 44.4 | 71 3 US-08-943-173-2 | Sequence 19, Appl |
| 12 | 36 | 44.4 | 181 4 US-09-117-257-19 | Sequence 19, Appl |
| 13 | 36 | 44.4 | 181 4 US-08-945-476-19 | Sequence 19, Appl |
| 14 | 36 | 44.4 | 181 4 US-09-489-352-19 | Sequence 19, Appl |
| 15 | 36 | 44.4 | 182 4 US-09-117-257-48 | Sequence 48, Appl |
| 16 | 36 | 44.4 | 182 4 US-09-489-352-48 | Sequence 48, Appl |
| 17 | 36 | 44.4 | 236 4 US-09-134-001C-3558 | Sequence 3558, Ap |
| 18 | 36 | 44.4 | 355 2 US-08-458-555-2 | Sequence 2, Appl |
| 19 | 36 | 44.4 | 610 1 US-07-821-717B-6 | Sequence 6, Appl |
| 20 | 36 | 44.4 | 610 1 US-08-119-252B-6 | Sequence 6, Appl |
| 21 | 36 | 44.4 | 610 1 US-08-135-929A-11 | Sequence 11, Appl |
| 22 | 36 | 44.4 | 610 1 US-08-234-265A-11 | Sequence 11, Appl |
| 23 | 36 | 44.4 | 2318 4 US-09-091-219-24 | Sequence 24, Appl |
| 24 | 35 | 43.2 | 136 4 US-08-936-165A-461 | Sequence 461, App |
| 25 | 35 | 43.2 | 223 4 US-09-009-816-4 | Sequence 4, Appl |
| 26 | 35 | 43.2 | 225 4 US-09-071-035-204 | Sequence 204, App |
| 27 | 35 | 43.2 | 267 4 US-08-818-112-142 | Sequence 142, App |

| | | | | |
|----|----|------|---------------------------|--------------------|
| 28 | 35 | 43.2 | 267 4 US-08-818-111-137 | Sequence 137, App |
| 29 | 35 | 43.2 | 267 4 US-09-056-556-142 | Sequence 142, App |
| 30 | 35 | 43.2 | 267 4 US-09-072-596-137 | Sequence 137, App |
| 31 | 35 | 43.2 | 285 4 US-09-071-035-202 | Sequence 202, App |
| 32 | 35 | 43.2 | 344 6 5210183-2 | Patent No. 5210183 |
| 33 | 35 | 43.2 | 367 4 US-09-009-816-2 | Sequence 2, Appl |
| 34 | 35 | 43.2 | 548 2 US-09-032-315-4 | Sequence 4, Appl |
| 35 | 35 | 43.2 | 548 2 US-08-993-318A-4 | Sequence 4, Appl |
| 36 | 35 | 43.2 | 548 4 US-09-399-886-4 | Sequence 4, Appl |
| 37 | 35 | 43.2 | 548 4 US-09-396-260-4 | Sequence 4, Appl |
| 38 | 35 | 43.2 | 558 4 US-09-576-281-4 | Sequence 4, Appl |
| 39 | 35 | 43.2 | 558 4 US-09-134-001C-4178 | Sequence 4178, Ap |
| 40 | 35 | 43.2 | 662 1 US-07-841-651-4 | Sequence 4, Appl |
| 41 | 35 | 43.2 | 683 6 5210183-3 | Patent No. 5210183 |
| 42 | 35 | 43.2 | 822 4 US-09-564-805-222 | Sequence 222, App |
| 43 | 35 | 43.2 | 826 4 US-09-564-805-2 | Sequence 2, Appl |
| 44 | 35 | 43.2 | 826 4 US-09-564-805-224 | Sequence 224, App |
| 45 | 35 | 43.2 | 826 4 US-09-564-805-226 | Sequence 226, App |

ALIGNMENTS

RESULT 1
US-08-194-338-12
Sequence 12, Application US/08194338
Patent No. 5474898
GENERAL INFORMATION:
APPLICANT: Ventier, John C.
APPLICANT: Fraser, Claire M.
APPLICANT: McCombie, William R.
TITLE OF INVENTION: OCTOPAMINE RECEPTOR
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelson, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-194-338-12
Query Match 50.6%; Score 41; DB 1; Length 788;
Best Local Similarity 52.9%; Pred. No. 50;

Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 EKTPLTTAAAPVYXNA 19

Db 602 EDOPTTTAAAPLASAA 618

RESULT 2

US-08-470-202-59

; Sequence 59, Application US/08470202

; Patent No. 5759808

; GENERAL INFORMATION:

; APPLICANT: Guerrier, Lutz G.

; APPLICANT: Eberle, Josef

; APPLICANT: Brunn, Albrecht V.

; APPLICANT: Knapp, Stefan

; APPLICANT: Hauser, Hans-Peter

; TITLE OF INVENTION: Retrovirus from the HIV Group and Its

; NUMBER OF SEQUENCES: 63

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESS: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,202

; FILING DATE: US

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/132,653

; FILING DATE: 05-OCT-1993

; APPLICATION NUMBER: DE P 42 33 646.5

; FILING DATE: 06-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 35 718.7

; FILING DATE: 22-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 44 541.8

; FILING DATE: 30-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 43 18 186.4

; FILING DATE: 01-JUN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Michael J. Blake

; REGISTRATION NUMBER: 37,096

; REFERENCE/DOCKET NUMBER: 05495-0001-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 498 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-470-202-59

; Query Match 49.4%; Score 40; DB 1; Length 498;

; Best Local Similarity 44.4%; Pred. No. 44;

; Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 EKTPLTTAAAPVYXNA 19

Db 119 EETSPROTSONYPIVTNA 136

Db 119 EETSPROTSONYPIVTNA 136

RESULT 3

US-08-471-770-59

; Sequence 59, Application US/08471770

; Patent No. 5770427

; GENERAL INFORMATION:

; APPLICANT: Guerrier, Lutz G.

; APPLICANT: Eberle, Josef

; APPLICANT: Brunn, Albrecht V.

; APPLICANT: Knapp, Stefan

; APPLICANT: Hauser, Hans-Peter

; TITLE OF INVENTION: Retrovirus from the HIV Group and Its

; NUMBER OF SEQUENCES: 63

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESS: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/471,770

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/132,653

; FILING DATE: 05-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 33 646.5

; FILING DATE: 06-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 35 718.7

; FILING DATE: 22-OCT-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 44 541.8

; FILING DATE: 30-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 43 18 186.4

; FILING DATE: 01-JUN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Carol P. Binaudi

; REGISTRATION NUMBER: 32,220

; REFERENCE/DOCKET NUMBER: 05495-0001-03000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 498 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-471-770-59

; Query Match 49.4%; Score 40; DB 1; Length 498;

; Best Local Similarity 44.4%; Pred. No. 44;

; Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 EKTPLTTAAAPVYXNA 19

Db 119 EETSPROTSONYPIVTNA 136

ATTORNEY/AGENT INFORMATION:
NAME: KEEBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747-063-2747
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-624-125-20

Query Match 45.7%; Score 37; DB 1; Length 456;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 9 TTAAXAPVYXNA 19
DB 336 TTAAPVYXNA 346

RESULT 7
US-08-679-635A-4
Sequence 4, Application US/08679635A
Patent No. 5985643

GENERAL INFORMATION:
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Hermenia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/679,635A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-487-5800
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-679-635A-4

Query Match 45.7%; Score 37; DB 2; Length 463;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 TTAAXAPVYXNA 19
DB 382 TTAAPVYXNA 393

RESULT 8
US-09-419-163-4
Sequence 4, Application US/09419163

Patent No. 6391614
GENERAL INFORMATION:
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Hermenia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/419,163
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/679,635
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-487-5800
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-419-163-4

Query Match 45.7%; Score 37; DB 4; Length 463;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 TTAAXAPVYXNA 19
DB 382 TTAAPVYXNA 393

RESULT 9
US-08-943-173-8
Sequence 8, Application US/08943173
Patent No. 6048538
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
APPLICANT: Shen, Fan
TITLE OF INVENTION: PEPTIDES DERIVED
TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS OF
TITLE OF INVENTION: FOOT AND MOUTH DISEASE VIRUS AS
TITLE OF INVENTION: DIAGNOSTIC REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0053

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,173
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin, Maria C. H.
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-943-173-8
;
Query Match      44.4% Score 36; DB 3; Length 19;
Best Local Similarity 53.3% Pred. No. 5;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 EKKPLTTAAKAPV 16
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 5 ERQKPLKVKAKAPV 19

RESULT 10
US-08-943-173-16
; Sequence 16, Application US/08943173
; Patent No. 6048538
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; APPLICANT: Shen, Fan
; APPLICANT: Chen, Pei De
; TITLE OF INVENTION: PEPTIDES DERIVED
; TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS OF
; TITLE OF INVENTION: FOOT AND MOUTH DISEASE VIRUS AS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C. H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,173
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin, Maria C. H.
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid

```

```

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-943-173-16
;
Query Match      44.4% Score 36; DB 3; Length 58;
Best Local Similarity 53.3% Pred. No. 18;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 EKKPLTTAAKAPV 16
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 31 ERQKPLKVKAKAPV 45

RESULT 11
US-08-943-173-2
; Sequence 2, Application US/08943173
; Patent No. 6048538
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang YI
; APPLICANT: Shen, Fan
; APPLICANT: Chen, Pei De
; TITLE OF INVENTION: PEPTIDES DERIVED
; TITLE OF INVENTION: FROM THE NON-STRUCTURAL PROTEINS OF
; TITLE OF INVENTION: FOOT AND MOUTH DISEASE VIRUS AS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C. H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,173
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin, Maria C. H.
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-943-173-2
;
Query Match      44.4% Score 36; DB 3; Length 71;
Best Local Similarity 53.3% Pred. No. 22;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 EKKPLTTAAKAPV 16
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 31 ERQKPLKVKAKAPV 45

RESULT 12
US-09-117-257-19
; Sequence 19, Application US/09117257
; Patent No. 6214355
; GENERAL INFORMATION:
; APPLICANT: Hook, Magnus
; APPLICANT: Guo, Betty

```

APPLICANT: Hanson, Mark
TITLE OF INVENTION: Dbpa AND dbpb COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4210.000500
CURRENT APPLICATION NUMBER: US/09/117,257
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: PCT/US96/17081
EARLIER FILING DATE: 1996-10-22
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 08/427,023
EARLIER FILING DATE: 1995-04-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 181
TYPE: PRT
ORGANISM: Borrelia afzelii
US-09-117-257-19

Query Match 44.4%; Score 36; DB 4; Length 181;
Best Local Similarity 47.1%; Pred. No. 65;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 3 EKTPLTTAAAXAPVYXNA 19
|||||
Db 139 EKTPTTAEGITTIYAKA 155

RESULT 13
US-08-945-476-19
Sequence 19, Application US/08945476
Patent No. 6248517

GENERAL INFORMATION:

APPLICANT: DECORIN BINDING PROTEIN COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,476
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/589,711
FILING DATE: 22-JAN-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/427,023
FILING DATE: 24-APR-1995
INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-945-476-19

Query Match 44.4%; Score 36; DB 4; Length 181;
Best Local Similarity 47.1%; Pred. No. 65;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 3 EKTPLTTAAAXAPVYXNA 19
|||||
Db 139 EKTPTTAEGITTIYAKA 155

RESULT 14
US-09-489-352-19
Sequence 19, Application US/09489352
Patent No. 6312907
GENERAL INFORMATION:

APPLICANT: Hook, Magnus
TITLE OF INVENTION: Dbpa AND dbpb COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4210.000500
CURRENT APPLICATION NUMBER: US/09/489,352
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/US96/17081
EARLIER FILING DATE: 1996-10-22
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 08/427,023
EARLIER FILING DATE: 1995-04-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 181
TYPE: PRT
ORGANISM: Borrelia afzelii
US-09-489-352-19

Query Match 44.4%; Score 36; DB 4; Length 181;
Best Local Similarity 47.1%; Pred. No. 65;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 3 EKTPLTTAAAXAPVYXNA 19
|||||
Db 139 EKTPTTAEGITTIYAKA 155

RESULT 15
US-09-117-257-48
Sequence 48, Application US/09117257
Patent No. 6214355

GENERAL INFORMATION:

APPLICANT: Hook, Magnus
TITLE OF INVENTION: DECORIN BINDING PROTEIN COMPOSITIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,257
FILING DATE: 1998-07-22
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US96/17081
FILING DATE: 1996-10-22
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 08/427,023
EARLIER FILING DATE: 1995-04-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,711
FILING DATE: 22-JAN-1996
INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:
LENGTH: 182
TYPE: PRT
ORGANISM: Borrelia afzelii
US-09-117-257-48

Query Match 44.4%; Score 36; DB 4; Length 182;
Best Local Similarity 47.1%; Pred. No. 65;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 3 EKTPLTTAAAXAPVYXNA 19
|||||
Db 139 EKTPTTAEGITTIYAKA 155

Search completed: March 14, 2003, 09:13:13
Job time : 15 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:12:34 ; Search time 13 Seconds

(without alignments)
67.365 Million cell updates/sec

Title: US-09-359-426c-2

Perfect score: 81

Sequence: 1 XEEKTPITTAAXAPVYXNA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------------------|-------------------|
| 1 | 41 | 50.6 | 132 | 12 US-10-078-929-22 | Sequence 22, Appl |
| 2 | 41 | 50.6 | 132 | 12 US-10-078-929-198 | Sequence 198, App |
| 3 | 40 | 49.4 | 445 | 10 US-09-815-242-11701 | Sequence 11701, A |
| 4 | 40 | 49.4 | 498 | 9 US-09-886-156-59 | Sequence 59, Appl |
| 5 | 40 | 49.4 | 498 | 9 US-09-886-150-59 | Sequence 59, Appl |
| 6 | 40 | 49.4 | 498 | 9 US-09-886-149-59 | Sequence 59, Appl |
| 7 | 40 | 49.4 | 498 | 9 US-09-886-159-59 | Sequence 59, Appl |
| 8 | 39 | 48.1 | 155 | 10 US-09-952-432A-2 | Sequence 2, Appl |
| 9 | 39 | 48.1 | 155 | 10 US-09-952-432A-16 | Sequence 16, Appl |
| 10 | 39 | 48.1 | 233 | 9 US-09-738-626-5663 | Sequence 5663, Ap |
| 11 | 39 | 48.1 | 395 | 10 US-09-952-432A-19 | Sequence 19, Appl |
| 12 | 39 | 48.1 | 395 | 10 US-09-952-432A-21 | Sequence 21, Appl |
| 13 | 38 | 46.9 | 229 | 10 US-09-866-562-92 | Sequence 52, Appl |
| 14 | 38 | 46.9 | 261 | 9 US-09-738-626-5209 | Sequence 5209, Ap |
| 15 | 38 | 46.9 | 277 | 10 US-09-764-846-214 | Sequence 214, App |
| 16 | 37 | 45.7 | 456 | 10 US-09-323-998D-20 | Sequence 20, Appl |
| 17 | 37 | 45.7 | 498 | 10 US-09-323-998D-57 | Sequence 57, Appl |
| 18 | 37 | 45.7 | 500 | 10 US-09-323-998D-58 | Sequence 58, Appl |
| 19 | 37 | 45.7 | 500 | 10 US-09-323-998D-59 | Sequence 59, Appl |

| | | | | | |
|----|------|------|-------|------------------------|-------------------|
| 20 | 36 | 44.4 | 501 | 10 US-09-323-998D-55 | Sequence 55, Appl |
| 21 | 35.5 | 43.8 | 175 | 10 US-09-925-301-964 | Sequence 964, App |
| 22 | 35 | 43.2 | 29 | 10 US-09-864-761-42235 | Sequence 42235, A |
| 23 | 35 | 43.2 | 136 | 10 US-09-939-980-461 | Sequence 461, App |
| 24 | 35 | 43.2 | 182 | 10 US-09-864-761-46598 | Sequence 46598, A |
| 25 | 35 | 43.2 | 156 | 9 US-09-738-626-6738 | Sequence 6738, Ap |
| 26 | 35 | 43.2 | 532 | 9 US-10-037-667-2 | Sequence 2, Appl |
| 27 | 35 | 43.2 | 548 | 9 US-09-869-877-4 | Sequence 4, Appl |
| 28 | 35 | 43.2 | 577 | 9 US-09-732-350-4 | Sequence 4, Appl |
| 29 | 35 | 43.2 | 822 | 9 US-09-988-626-3648 | Sequence 3648, Ap |
| 30 | 35 | 43.2 | 822 | 9 US-09-988-626-222 | Sequence 222, App |
| 31 | 35 | 43.2 | 826 | 9 US-09-988-626-222 | Sequence 222, App |
| 32 | 35 | 43.2 | 826 | 9 US-09-988-626-224 | Sequence 224, App |
| 33 | 35 | 43.2 | 826 | 9 US-09-988-626-224 | Sequence 224, App |
| 34 | 35 | 43.2 | 826 | 9 US-09-988-626-226 | Sequence 226, App |
| 35 | 35 | 43.2 | 826 | 9 US-09-988-626-226 | Sequence 226, App |
| 36 | 35 | 43.2 | 826 | 9 US-09-988-626-226 | Sequence 226, App |
| 37 | 35 | 43.2 | 826 | 9 US-09-988-626-224 | Sequence 224, App |
| 38 | 35 | 43.2 | 826 | 9 US-09-988-626-224 | Sequence 224, App |
| 39 | 35 | 43.2 | 2993 | 9 US-09-988-626-6239 | Sequence 6239, Ap |
| 40 | 35 | 43.2 | 4613 | 9 US-09-861-289-31 | Sequence 31, Appl |
| 41 | 35 | 43.2 | 4613 | 9 US-09-861-289-31 | Sequence 31, Appl |
| 42 | 35 | 43.2 | 11877 | 9 US-09-861-289-6 | Sequence 6, Appl |
| 43 | 35 | 43.2 | 11877 | 9 US-09-861-289-6 | Sequence 6, Appl |
| 44 | 34 | 42.0 | 83 | 10 US-09-864-761-44350 | Sequence 44350, A |
| 45 | 34 | 42.0 | 86 | 9 US-09-847-102A-136 | Sequence 136, App |
| | | | 155 | 10 US-09-952-432A-17 | Sequence 17, Appl |

ALIGNMENTS

RESULT 1
US-10-078-929-22
Sequence 22, Application US/10078929
Patent No. US20020152497A1
GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo O.
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078, 929
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
SEQ ID NO 22
LENGTH: 132
TYPE: PRT

ORGANISM: Oryza sativa
US-10-078-929-22

Query Match 50.6%; Score 41; DB 12; Length 132;
Best Local Similarity 50.0%; Pred. No. 3.6;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 2 EKKPLTTAAAXAPVYXNA 19
DB 97 EAAPPTTAAEAAPATAAA 114

RESULT 2
US-10-078-929-198
Sequence 198, Application US/10078929
Patent No. US20020152497A1
GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo O.
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
FILE REFERENCE: B01357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
SEQ ID NO 198
LENGTH: 132
TYPE: PRT
ORGANISM: Oryza sativa
US-10-078-929-198

Query Match 50.6%; Score 41; DB 12; Length 132;
Best Local Similarity 50.0%; Pred. No. 3.6;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 2 EKKPLTTAAAXAPVYXNA 19
DB 97 EAAPPTTAAEAAPATAAA 114

RESULT 3
US-09-815-242-11701
Sequence 11701, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11701
LENGTH: 445
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-815-242-11701

Query Match 49.4%; Score 40; DB 10; Length 445;
Best Local Similarity 57.1%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 EKKPLTTAAAXAPV 15
DB 382 EKKPLTTAAADMAAI 395

RESULT 4
US-09-886-156-59
Sequence 59, Application US/09886156
Patent No. US20020155428A1
GENERAL INFORMATION:
APPLICANT: Guertler, Lutz G.
APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
CURRENT APPLICATION NUMBER: US/09/886,156
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US/09/109,916
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: DE P 42 33 646.5
PRIOR FILING DATE: 1992-10-06
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR FILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR FILING DATE: 1992-12-30
PRIOR APPLICATION NUMBER: DE P 43 18 186.4
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59
LENGTH: 498
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-09-886-156-59

Query Match 49.4%: Score 40; DB 9; Length 498;
Best Local Similarity 44.4%: Pred. No. 25;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EEXTPLTTAAAXAPVYXNA 19
DB 119 EETSPROTSONYPIVTNA 136

RESULT 5
US-09-886-150-59

; Sequence 59, Application US/09886150
; Patent No. US20020172939A1
; GENERAL INFORMATION:
; APPLICANT: Guerlier, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,150
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 59
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-09-886-150-59

Query Match 49.4%: Score 40; DB 9; Length 498;
Best Local Similarity 44.4%: Pred. No. 25;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EEXTPLTTAAAXAPVYXNA 19
DB 119 EETSPROTSONYPIVTNA 136

RESULT 6
US-09-886-149-59
; Sequence 59, Application US/09886149
; Publication No. US20030003442A1
; GENERAL INFORMATION:
; APPLICANT: Guerlier, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,149
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30

; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 59
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-09-886-149-59

Query Match 49.4%: Score 40; DB 9; Length 498;
Best Local Similarity 44.4%: Pred. No. 25;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EEXTPLTTAAAXAPVYXNA 19
DB 119 EETSPROTSONYPIVTNA 136

RESULT 7
US-09-886-159-59
; Sequence 59, Application US/09886159
; Publication No. US20030003443A1
; GENERAL INFORMATION:
; APPLICANT: Guerlier, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,159
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US/09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentl Ver. 2.0
; SEQ ID NO 59
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-09-886-159-59

Query Match 49.4%: Score 40; DB 9; Length 498;
Best Local Similarity 44.4%: Pred. No. 25;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 2 EEXTPLTTAAAXAPVYXNA 19
DB 119 EETSPROTSONYPIVTNA 136

RESULT 8
US-09-952-432A-2
; Sequence 2, Application US/09952432A
; Patent No. US20020150588A1
; GENERAL INFORMATION:
; APPLICANT: Allison, James P.
; APPLICANT: Fassio, Marcelia
; APPLICANT: Snastr, Nilabh
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
; FILE REFERENCE: 018941-001110US
; CURRENT APPLICATION NUMBER: US/09/952,432A
; PRIOR FILING DATE: 2002-04-15

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CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 5663
LENGTH: 233
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-5663

Query Match      48.1%; Score 39; DB 9; Length 233;
Best Local Similarity 66.7%; Pred. NO. 16;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 TPLTTAAXAPV 16
      |||::|||
Db      35 TPTTSASPAV 46

RESULT 11
US-09-952-432A-19
Sequence 19, Application US/09952432A
Patent No. US20020150588A1
GENERAL INFORMATION:
APPLICANT: Allison, James P.
APPLICANT: Shastri, Nilabh
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
FILE REFERENCE: 018941-001110US
CURRENT APPLICATION NUMBER: US/09/952,432A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/234,472
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 395
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Tumor SPAS-1
US-09-952-432A-19

Query Match      48.1%; Score 39; DB 10; Length 395;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 TPLTTAAXAPV 16
      :|||::|||
Db      300 SPTTAATMPV 311

RESULT 12
US-09-952-432A-21
Sequence 21, Application US/09952432A
Patent No. US20020150588A1
GENERAL INFORMATION:
APPLICANT: Allison, James P.
APPLICANT: Fasso, Marcella
APPLICANT: Shastri, Nilabh
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
FILE REFERENCE: 018941-001110US
CURRENT APPLICATION NUMBER: US/09/952,432A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/234,472

```


;; PRIOR FILING DATE: 2000-09-21
;; NUMBER OF SEQ ID NOS: 32
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 21
;; LENGTH: 395
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: No. US20020150588A1mal SPAS-1
US-09-952-432A-21

Query Match 48.18; Score 39; DB 10; Length 395;
Best Local Similarity 66.7%; Pred. No. 29;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 TPLTTAAAPV 16
DB 300 SPTTTATMPV 311

RESULT 13

US-09-866-562-92
;; Sequence 92, Application US/09866562
;; Patent No. US2002009758A1
;; GENERAL INFORMATION:
;; APPLICANT: Harlocker, Susan L.
;; APPLICANT: Wang, Tonglong
;; APPLICANT: Bangur, Chaitanya S.
;; APPLICANT: Klee, Jennifer
;; APPLICANT: Switzer, Anne
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;; FILE REFERENCE: 210121.502
;; CURRENT APPLICATION NUMBER: US/09/866.562
;; CURRENT FILING DATE: 2001-05-25
;; NUMBER OF SEQ ID NOS: 96
;; SEQ ID NO 92
;; LENGTH: 229
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-866-562-92

Query Match 46.9%; Score 38; DB 10; Length 229;
Best Local Similarity 39.3%; Pred. No. 23;
Matches 11; Conservative 1; Mismatches 4; Indels 12; Gaps 1;

OY 3 EKTPLTTAA-----XAPVYXN 18
DB 109 EKTPLKTTATPLSLPKPRMDTAPVVAS 136

RESULT 14

US-09-738-626-5209
;; Sequence 5209, Application US/09738626
;; Publication No. US20020197605A1
;; GENERAL INFORMATION:
;; APPLICANT: NAKAGAWA, SATOSHI
;; APPLICANT: MIZOGUCHI, HIROSHI
;; APPLICANT: ANDO, SEIKO
;; APPLICANT: HAYASHI, MIKIRO
;; APPLICANT: OCHIAI, KEIJI
;; APPLICANT: YOKOI, HARUHIKO
;; APPLICANT: TATEISHI, NAKO
;; APPLICANT: SENOH, AKIHITO
;; APPLICANT: IKEDA, MASATO
;; APPLICANT: OZAKI, AKIO
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-125
;; CURRENT APPLICATION NUMBER: US/09/738.626
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: JP 99/377484
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: JP 00/159162

;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: JP 00/280988
;; PRIOR FILING DATE: 2000-08-03
;; NUMBER OF SEQ ID NOS: 7059
;; SOFTWARE: PatentIn ver. 3.0
;; SEQ ID NO 5209
;; LENGTH: 261
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5209

Query Match 46.9%; Score 38; DB 9; Length 261;
Best Local Similarity 70.0%; Pred. No. 27;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 PLTTAAAPV 15
DB 149 PLTTAASAPV 158

RESULT 15

US-09-764-846-214
;; Sequence 214, Application US/09764846
;; Patent No. US20020102638A1
;; GENERAL INFORMATION:
;; APPLICANT: Rosen et al.
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;; FILE REFERENCE: PT212
;; CURRENT APPLICATION NUMBER: US/09/764.846
;; CURRENT FILING DATE: 2001-01-17
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 348
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 214
;; LENGTH: 277
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (6)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (7)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (8)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (254)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (261)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (268)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (275)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;; NAME/KEY: SITE
;; LOCATION: (277)
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-214

Query Match 46.9%; Score 38; DB 10; Length 277;
Best Local Similarity 46.7%; Pred. No. 29;

Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 5 TPLTTAAAPVYXNA 19
DB 120 JPVRAAASPIVGA 134

Fri Mar 14 09:30:10 2003

us-09-359-426c-2.rapb

Search completed: March 14, 2003, 09:16:49
Job time : 14 secs

GenCore version 5.1.4.P5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:10:24 ; Search time 18 Seconds

(without alignments)
101.475 Million cell updates/sec

Title: US-09-359-426c-2

Perfect score: 81

Sequence: 1 XEKTPLTTAAKAPVYXNA 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR73:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 63 | 77.8 | 482 | 2 B83113 | catalase PA4236 (I |
| 2 | 53 | 65.4 | 484 | 2 A58663 | catalase (EC 1.11. |
| 3 | 48 | 59.3 | 480 | 2 AB0148 | catalase (EC 1.11. |
| 4 | 46 | 56.8 | 262 | 2 T33408 | hypothetical prote |
| 5 | 45 | 56.6 | 128 | 2 E88400 | protein H34124.2 (|
| 6 | 45 | 55.6 | 128 | 2 JCI273 | ribosomal protein |
| 7 | 44 | 54.3 | 306 | 2 AE0963 | probable carboxydr |
| 8 | 44 | 54.3 | 427 | 2 F85436 | hypothetical prote |
| 9 | 43 | 53.1 | 483 | 2 S37055 | catalase (EC 1.11. |
| 10 | 42 | 51.9 | 105 | 2 A44639 | catalase (EC 1.11. |
| 11 | 42 | 51.9 | 321 | 2 T08462 | hypothetical prote |
| 12 | 42 | 51.9 | 436 | 2 T46107 | hypothetical prote |
| 13 | 41 | 50.6 | 132 | 2 T50779 | hypothetical prote |
| 14 | 41 | 50.6 | 482 | 2 S60757 | copper chaperone h |
| 15 | 40 | 49.4 | 171 | 2 T31478 | catalase (EC 1.11. |
| 16 | 40 | 49.4 | 252 | 2 H72469 | hypothetical prote |
| 17 | 40 | 49.4 | 258 | 2 AD1328 | hypothetical prote |
| 18 | 40 | 49.4 | 394 | 2 E87611 | hypothetical prote |
| 19 | 40 | 49.4 | 788 | 2 S05661 | muscarinic acetylch |
| 20 | 40 | 49.4 | 1360 | 2 T31674 | hypothetical prote |
| 21 | 39.5 | 48.8 | 405 | 2 JQ2147 | OHP1 protein - mai |
| 22 | 39 | 48.1 | 486 | 2 S10772 | 2-hydroxyisovaleryl |
| 23 | 39 | 48.1 | 507 | 2 B87400 | aldehyde dehydroge |
| 24 | 39 | 48.1 | 527 | 2 S46088 | hypothetical prote |
| 25 | 39 | 48.1 | 1353 | 2 T26301 | hypothetical prote |
| 26 | 38.5 | 47.5 | 1658 | 2 D75489 | growth-blocking pe |
| 27 | 38 | 46.9 | 143 | 2 S68226 | cytochrome c1, hem |
| 28 | 38 | 46.9 | 307 | 2 T40089 | phospholipase D (E |
| 29 | 38 | 46.9 | 307 | 2 A35125 | |

| | | | | | |
|----|------|------|------|----------|--------------------|
| 30 | 38 | 46.9 | 348 | 2 S40750 | hypothetical prote |
| 31 | 38 | 46.9 | 474 | 2 E87650 | peptidase, M20/M25 |
| 32 | 38 | 46.9 | 532 | 2 S40983 | hypothetical prote |
| 33 | 38 | 46.9 | 573 | 2 F81313 | peptidase (M3 faml |
| 34 | 38 | 46.9 | 684 | 2 T25603 | hypothetical prote |
| 35 | 38 | 46.9 | 695 | 2 D71283 | probable transla |
| 36 | 38 | 46.9 | 747 | 2 F88561 | protein F58A4.11 (|
| 37 | 38 | 46.9 | 1679 | 2 S48385 | hypothetical prote |
| 38 | 37.5 | 46.3 | 200 | 2 G86194 | hypothetical prote |
| 39 | 37 | 45.7 | 71 | 2 F72332 | hypothetical prote |
| 40 | 37 | 45.7 | 116 | 2 C83492 | hypothetical prote |
| 41 | 37 | 45.7 | 328 | 2 T01225 | hypothetical prote |
| 42 | 37 | 45.7 | 347 | 2 T35518 | probable secreted |
| 43 | 37 | 45.7 | 463 | 2 S72992 | probable phosphory |
| 44 | 37 | 45.7 | 488 | 2 T42038 | catalase (EC 1.11. |
| 45 | 37 | 45.7 | 500 | 2 S72505 | lycopen beta-cycl |

ALIGNMENTS

RESULT 1.

B83113

Catalase PA4236 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: B83113

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lathig, K.; I

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: AB2950; MUID:20437337; PMID:10944043

A:Accession: B83113

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-482 <STO>

A:Cross-references: GB:AE004841; GB:AE004091; NID:9950451; PIDN:AAG07624.1; GSPDB:GN

C:Genetics:

A:Gene: katA; PA4236

C:Superfamily: catalase

Query Match

Best Local Similarity 77.8%; Score 63; DB 2; Length 482;

Matches 14; Conservativity 82.4%; Pred. No. 0.0041;

Mismatches 0; Indels 3; Gaps 0;

QY 2 EKTPLTTAAKAPVYXN 18

DB 2 EKTPLTTAAKAPVYDN 18

RESULT 2

A58663

Catalase (EC 1.11.1.6) [validated] - Proteus mirabilis

C:Species: Proteus mirabilis

A:Variety: strain PR, peroxide resistant

C>Date: 19-Nov-1997 #sequence_revision 21-Nov-1997 #text_change 15-Sep-2000

C:Accession: A58663; B58663

R:Buy, A.; Brach, V.; Sterjades, R.; Chroboczek, J.; Thibault, P.; Gagnon, J.; Jc

J. Protein Chem. 14, 59-72, 1995

A:Title: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of

A:Reference number: A58663; MUID:95305957; PMID:7786407

A:Accession: A58663

A:Molecule type: protein

A:Residues: 1-484 <BUZ1>

A:Accession: B58663

A:Molecule type: DNA

A:Residues: 1-305, 'AE' <BUZ2>

R:Goulet, P.; Jouve, H.M.; Dideberg, O.

submitted to the Brookhaven Protein Data Bank, June 1996

A:Reference number: A67899; PDB:2CAE

A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 3-475

R:Gouet, P.; Jouve, H.M.; Hajdu, J.
 Submitted to the Brookhaven Protein Data Bank, June 1996
 A:Reference number: A67900; PDB:2CAF
 A:Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
 A:Note: compound 1
 R:Gouet, P.; Jouve, H.M.; Hajdu, J.
 Submitted to the Brookhaven Protein Data Bank, June 1996
 A:Reference number: A67901; PDB:2CAG
 A:Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
 A:Note: compound II, dithiothreitol reduced compound I
 R:Gouet, P.; Jouve, H.M.; Dideberg, O.
 Submitted to the Brookhaven Protein Data Bank, July 1996
 A:Reference number: A67902; PDB:2CAH
 A:Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
 A:Note: native Fe(III) with NADPH
 R:Gouet, P.; Jouve, H.M.; Dideberg, O.
 J. Mol. Biol. 249, 933-954, 1995
 A:Title: Crystal structure of Proteus mirabilis PR catalase with and without bound NADPH
 A:Reference number: A58654; MUID:9531317; PMID:7791219
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms
 A:Complex: homotetramer
 A:Function:
 A:Description: catalyzes the conversion of two of molecules of hydrogen peroxide to two
 A:Note: this enzyme has a tightly bound NADPH cofactor
 C:Superfamily: catalase
 C:Keywords: chromoprotein; heme; homotetramer; iron; metalloprotein; NADP; oxidoreductas
 F:53/Modified site: methionine sulfone (Met) #status experimental
 F:54_93_127/Active site: His, Ser, Asn #status predicted
 F:337/Binding site: heme iron (Tyr) (axial ligand) #status experimental

Query Match 65.4%; Score 53; DB 2; Length 484;
 Best Local Similarity 75.0%; Pred. No. 0.22;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 EKTPLTTAAAPVYXN 18
 |||||
 Db 2 EKKKLTAAAGAPVVDN 17

RESULT 3
 AB0148
 catalase (EC 1.11.1.6) [imported] - Yersinia pestis (strain CO92)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AB0148
 R:Parfhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Figure 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360
 A:Accession: AB0148
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-480 <CUR>
 A:Cross-references: GB:AL590842; PIDN:CAC90045.1; PID:g15979266; GSPDB:GN00175
 C:Genetics:
 A:Gene: kata
 C:Superfamily: catalase
 C:Keywords: oxidoreductase

Query Match 59.3%; Score 48; DB 2; Length 480;
 Best Local Similarity 68.8%; Pred. No. 1.6;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 EKTPLTTAAAPVYXN 18
 |||||
 Db 4 KKKGLTTAAGAPVVDN 19

RESULT 4
 T33408
 hypothetical protein H34124.2 - Caenorhabditis elegans (fragment)

C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T33408
 R:Latrelle, P.; Wamsley, P.; O'Brien, D.
 Submitted to the EMBL Data Library, July 1998
 A:Description: The sequence of C. elegans cosmid H34124.
 A:Reference number: Z21340
 A:Accession: T33408
 A:Status: preliminary; translated from GB/EMBL/DDBT
 A:Molecule type: DNA
 A:Residues: 1-262 <LAT>
 A:Cross-references: EMBL:AF078784; PIDN:AAC26925.1; GSPDB:GN00021; CESP:H34124.2
 A:Experimental source: strain Bristol N2; clone H34124
 C:Genetics:
 A:Gene: CESP:H34124.2
 A:Map position: 3
 A:Note: Intron positions not resolved (incomplete sequence)

Query Match 56.8%; Score 46; DB 2; Length 262;
 Best Local Similarity 56.2%; Pred. No. 1.9;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 KTPLTTAAAPVYXNA 19
 |||||
 Db 190 KPLTSGSSARVYINNA 205

RESULT 5
 E88400
 Protein H34124.2 [imported] - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: E88400
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
 A:Reference number: A75000; MUID:99065613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C-
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
 A:Accession: E88400
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-262 <STO>
 A:Cross-references: GB:chr_III; PIDN:AAC26925.1; PID:g3329614; GSPDB:GN00021; CESP:H3
 C:Genetics:
 A:Gene: H34124.2
 A:Map position: 3

Query Match 56.8%; Score 46; DB 2; Length 262;
 Best Local Similarity 56.2%; Pred. No. 1.9;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 KTPLTTAAAPVYXNA 19
 |||||
 Db 190 KPLTSGSSARVYINNA 205

RESULT 6
 JCI273
 ribosomal protein L7/L12 - Streptomyces antibioticus
 C:Species: Streptomyces antibioticus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: JCI273
 R:Parra, F.; Blanco, G.; Alonso, J.M.M.; Balbin, M.; Mendez, C.; Salas, J.A.
 Gene 118, 127-129, 1992
 A:Title: Cloning and sequence of a gene encoding the L7/L12 ribosomal protein equiva
 A:Reference number: JCI273; MUID:92380478; PMID:1511874
 A:Accession: JCI273
 A:Molecule type: DNA
 A:Residues: 1-128 <PAR>
 A:Cross-references: GB:M89911; MUID:g153436; PIDN:AAA26811.1; PID:g153438
 C:Superfamily: Escherichia coli ribosomal protein L12
 C:Keywords: protein biosynthesis; ribosome

Query Match 55.6%: Score 45; DB 2; Length 128;
Best Local Similarity 66.7%: Pred. No. 1.3;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 2 EEXPLTTAAAXAPV 16
Db 28 EEXFDVTAAAAAPV 42

RESULT 7

AE0963

probable carbohydrate kinase STY3989 [imported] - *Salmonella enterica* subsp. *enterica* se

C:Species: *Salmonella enterica* subsp. *enterica* serovar Typhl

A:Note: this species has also been called *Salmonella typhi*

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

C:Accession: AE0963

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Garra, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A>Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* sero

A:Reference number: AB0502; PMID:11677608

A:Accession: AE0963

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-306 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03201.1; PID:q16504832; GSPDB:GN00176

C:Genetics:

A:Gene: STY3989

C:Superfamily: ribokinase

Query Match 54.3%: Score 44; DB 2; Length 306;
Best Local Similarity 47.1%: Pred. No. 4.9;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 3 EEXPLTTAAAXAPVXNA 19
Db 84 EKVCTTSGVAPLTVNA 100

RESULT 8

F85436

hypothetical protein AT4936970 [imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001

C:Accession: F85436

R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin

Nature 402, 769-777, 1999

A>Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.

A:Reference number: AB5001; MUID:20083488; PMID:10617198

A:Accession: F85436

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-427 <STO>

A:Cross-references: GB:NC_001268; NID:97270646; PIDN:CAB80363.1; GSPDB:GN00140

C:Genetics:

A:Gene: AT4936970

A:Map position: 4

Query Match 54.3%: Score 44; DB 2; Length 427;
Best Local Similarity 60.0%: Pred. No. 7.1;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 EEXPLTTAAAXAPV 16
Db 208 EKAEMTTAMQSPV 222

RESULT 9

S37055

catalase (EC 1.11.1.6) alpha-2 chain - *Streptomyces violaceus*

C:Species: *Streptomyces violaceus*

C:Date: 10-Dec-1993 #sequence_revision 26-May-1995 #text_change 04-Mar-2000

C:Accession: S37055

R:Facey, S.; Van Pee, K.H.; Vining, L.C.

submitted to the EMBL Data Library, August 1993

A:Reference number: S37055

A:Accession: S37055

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-483 <PAC>

A:Cross-references: EMBL:X74791; NID:9397888; PIDN:CAA52796.1; PID:9581780

A:Note: the source is designated as *Streptomyces venezuelae*

C:Genetics:

A:Start codon: GTG

C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase

F:54,93,127/Active site: His, Ser, Asn #status predicted

F:137/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match

Best Local Similarity 53.1%: Score 43; DB 2; Length 483;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 6 PLTTAAAXAPVXN 18
Db 5 PLTTAGAPVADN 17

RESULT 10

A4639

catalase (EC 1.11.1.6) - *Streptomyces coelicolor* (fragments)

C:Species: *Streptomyces coelicolor*

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 31-Oct-1997

C:Accession: A4639

R:Walker, G.

submitted to the Protein Sequence Database, September 1994

A:Reference number: A4639

A:Accession: A4639

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-105 <WAL>

C:Superfamily: catalase

C:Keywords: oxidoreductase

Query Match 51.9%: Score 42; DB 2; Length 105;
Best Local Similarity 69.2%: Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 6 PLTTAAAXAPVXN 18
Db 7 PLTTVAGAPVADN 19

RESULT 11

T08462

hypothetical protein F2206.250 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999

C:Accession: T08462

R:Queller, F.; Purnelle, B.; Boutry, M.; Goffeau, A.; Salanoubat, M.; Meves, H.W.; Ma

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16420

A:Accession: T08462

A:Molecule type: DNA

A:Residues: 1-321 <QUE>

A:Cross-references: EMBL:AL050300; GSPDB:GN00061; ATSP:F2206.250

A:Experimental source: cultivar Columbia; BAC clone F2206

C:Genetics:

A:Gene: ATSP:F2206.250

A:Map position: 3

Query Match 51.9%: Score 42; DB 2; Length 321;
Best Local Similarity 50.0%: Pred. No. 12;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 EEKPLTTAAXAPVYXNA 19

Db 291 EEKTPVEKKTGVVYKKA 308

RESULT 12

T46107
hypothetical protein T25B15.140 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T46107

R:Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, K.

submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23021

A:Accession: T46107

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-436 <ALC>

A:Cross-references: EMBL:AL132972

Experimental source: cultivar Columbia; BAC clone T25B15

C:Genetics:

A:Map position: 3

A:Introns: 418/1

A>Note: T25B15.140

Query Match

Best Local Similarity 51.9%; Score 42; DB 2; Length 436;
Best Local Similarity 50.0%; Pred. No. 16;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 EEKPLTTAAXAPVYXNA 19

Db 395 EEKTPVEKKTGVVYKKA 412

RESULT 13

T50779
copper chaperone homolog CCH [imported] - rice

C:Species: Oryza sativa (rice)

C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C:Accession: T50779

R:Himelblau, E.; Mira, H.; Jan, S.J.; Culotta, V.C.; Penarrubia, L.; Amasino, R.M.

Plant Physiol. 117, 1227-1234, 1998

A:Title: Identification of a functional homolog of the yeast copper homeostasis gene ATX

A:Reference number: Z24450; PMID:9701579

A:Accession: T50779

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-132 <HIM>

A:Cross-references: EMBL:AF198626; PIDN:AAF15285.1

Query Match

Best Local Similarity 50.6%; Score 41; DB 2; Length 132;
Best Local Similarity 50.0%; Pred. No. 6.5;

Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 EEKPLTTAAXAPVYXNA 19

Db 97 EAAPPTTAAPAAIAAA 114

RESULT 14

S60757
catalase (EC 1.11.1.6) - Bordetella pertussis

C:Species: Bordetella pertussis

C>Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000

C:Accession: S60757

R:Deshaizer, D.; Wood, G.E.; Friedman, R.L.

Mol. Microbiol. 14, 123-130, 1994

A:Title: Molecular characterization of catalase from Bordetella pertussis: identification

A:Reference number: S60757; PMID:9511725; PMID:7830550

A:Accession: S60757

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-482 <DES>

A:Cross-references: EMBL:U07800; NID:9494943; PIDN:AA18481.1; PID:9494944

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994

C:Genetics:

A:Gene: cata

C:Superfamily: catalase

C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase

F;57,96,130/Active site: His, Ser, Asn #status predicted

F;340/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match

Best Local Similarity 50.6%; Score 41; DB 2; Length 482;
Best Local Similarity 75.0%; Pred. No. 27;

Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 LTTAAAPVYXN 18

Db 9 LTTAAGAPVADN 20

RESULT 15

T31478
hypothetical protein F56F12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T31478

R:Ainscough, R.

submitted to the EMBL Data Library, October 1999

A:Reference number: Z21039

A:Accession: T31478

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-171 <WIL>

A:Cross-references: EMBL:Z82273; PIDN:CAB54978.1; GSPDB:GN00022; CESP:F56F12.1

A:Experimental source: clone F56F12

C:Genetics:

A:Gene: CESP:F56F12.1

A:Map position: 4

A:Introns: 16/2; 50/1

Query Match

Best Local Similarity 49.4%; Score 40; DB 2; Length 171;
Best Local Similarity 53.3%; Pred. No. 13;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 TPLTTAAXAPVYXNA 19

Db 73 TPTTTAAPAAIAA 87

Search completed: March 14, 2003, 09:12:52

Job time : 21 secs


```

DR InterPro: IPR002226; Catalase.
DR Pfam: PF00199; catalase.1.
DR PRINTS: PR00067; CATALASE.
DR PRODOM: PD000510; Catalase.1.
DR PROSITE: PS00437; CATALASE_1; 1.
DR PROSITE: PS00438; CATALASE_2; 1.
KM Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
KW Complete proteome.
FT ACT SITE 55 55 BY SIMILARITY.
FT ACT SITE 128 128 BY SIMILARITY.
FT BINDING 338 338 PROXIMAL HEME LIGAND (BY SIMILARITY).
SQ SEQUENCE 482 AA; 55589 MW; 845BAA647CAB414 CRC64;

Query Match
Best Local Similarity 77.8%; Score 63; DB 1; Length 482;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 EEKPLTTAAKAPVYVN 18
DB 2 EEKRLTTAAKAPVVDN 18

RESULT 2
ID CATA_PROM1 STANDARD: PRT; 484 AA.
AC P42321;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Catalase (EC 1.11.1.6).
GN KATA.
OS proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE, AND SEQUENCE OF 1-305 FROM N.A.
RC STRAIN=PR;
RX MEDLINE=95305957; PubMed=7786407;
RA Buzy A., Bracchi V., Steriades R., Chroboczek J., Thibault P.,
RA Gagnon J., Jouve H.-M., Hudry-Clergeon G.;
RT "Complete amino acid sequence of Proteus mirabilis PR catalase.
RT occurrence of a methionine sulfone in the close proximity of the
RT active site."
RT J. Protein Chem. 14:59-72(1995).
RL [2]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RP STRAIN=PR;
RC MEDLINE=95311317; PubMed=7791219;
RC Gouet P., Jouve H.-M., Dideberg O.;
RT "Crystal structure of Proteus mirabilis PR catalase with and without
RT bound NADPH."
RT J. Mol. Biol. 249:933-954(1995).
CC -1- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES
CC TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
CC -1- COFACTOR: HEME GROUP AND NADP.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MASS SPECTROMETRY: MW=55643; MW_ERR=5; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
DR PDB: 2CAE; 08-DEC-96.
DR PDB: 2CAF; 07-DEC-96.
DR PDB: 2CAG; 07-DEC-96.
DR PDB: 2CAH; 11-JAN-97.
DR InterPro: IPR002226; Catalase.
DR Pfam: PF00199; catalase.1.
DR PRINTS: PR00067; CATALASE.
DR PRODOM: PD000510; Catalase.1.
DR PROSITE: PS00437; CATALASE_1; 1.
DR PROSITE: PS00438; CATALASE_2; 1.
KM Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP;
KW 3D-structure.

```

```

FT MOD_RES 53 53 METHIONINE SULFONE.
FT ACT SITE 54 54
FT ACT SITE 127 127
FT BINDING 337 337 PROXIMAL HEME LIGAND.
SQ SEQUENCE 484 AA; 55614 MW; ADC25F3C41F5C50 CRC64;

Query Match
Best Local Similarity 65.4%; Score 53; DB 1; Length 484;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 EEKPLTTAAKAPVYVN 18
DB 2 EEKRLTTAAKAPVVDN 17

RESULT 3
ID RL7_STRAT STANDARD: PRT; 128 AA.
AC P29342;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L7/L12.
GN RPL7.
OS Streptomyces antibioticus.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92380478; PubMed=1511874;
RA Parra F., Blanco G., Alonso J.M., Balbin M., Mendez C., Salas J.A.;
RT "Cloning and sequence of a gene encoding the L7/L12 ribosomal protein
RT equivalent of Streptomyces antibioticus."
RT Gene 118:127-129(1992).
CC -1- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS
CC INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR
CC ACCURATE TRANSLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: M89911; AAA26811.1; -.
DR PIR: JCI273; JCI273.
DR HSSP: P02392; ICTF.
DR InterPro: IPR000206; Ribosomal_L12.
DR Pfam: PF00542; Ribosomal_L12; 1.
DR PRODOM: PD001326; Ribosomal_L12; 1.
DR TIGRFAMs: TIGR00855; L12; 1.
KM Ribosomal protein.
SQ SEQUENCE 128 AA; 13272 MW; F5C3E4F45D606E8 CRC64;

Query Match
Best Local Similarity 55.6%; Score 45; DB 1; Length 128;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 EEKPLTTAAKAPV 16
DB 28 EEKEDVTTAAKAPV 42

RESULT 4
ID BCA_STRVL STANDARD: PRT; 483 AA.
AC P33569;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)

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CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
-----
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-----
CC DR EMBL; U07800; AAA18481.1; -.
CC DR HSSP; P42321; 2CAE.
CC DR InterPro; IPR002226; Catalase.
CC DR Pfam; PF00199; catalase; 1.
CC DR PRINTS; PR00067; CATALASE.
CC DR ProDom; PD000510; Catalase; 1.
CC DR PROSITE; PS00437; CATALASE_1; 1.
CC DR PROSITE; PS00438; CATALASE_2; 1.
CC KM Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
CC FT ACT_SITE 57 57 BY SIMILARITY.
CC FT BINDING 130 130 PROXIMAL HEME LIGAND (BY SIMILARITY).
CC FT BINDING 340 340
CC SQ SEQUENCE 482 AA; 54508 MW; 7CB73E08975C219F CRC64;
-----
QY Query Match 50.6%; Score 41; DB 1; Length 482;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
-----
DB 7 LTTHAXAPVYN 18
||||| |
9 LTTHAGAPVDN 20
-----
RESULT 6
ACM1_DROME STANDARD: PRT; 722 AA.
ID ACM1_DROME
PI6395:
DT 01-AUG-1990 (rel. 15 Created)
DT 01-AUG-1990 (rel. 15; Last sequence update)
DT 01-NOV-1997 (rel. 35; Last annotation update)
DE Muscarinic acetylcholine receptor DML.
DI ACRC OR MACR-60C.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Peerygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Epiphytoidae; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
(1)
RN RP SEQUENCE FROM N.A.
RN RC STRAIN-Oregon-R;
RX MEDLINE=90046926; PubMed=2510174;
RA Shapiro R.A., Wakimoto B.T., Subers E.M., Nathanson N.M.;
RA Characterization and functional expression in mammalian cells of
RT genomic and cDNA clones encoding a Drosophila muscarinic
RT acetylcholine receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9039-9043(1989).
(2)
RN RP SEQUENCE FROM N.A.
RX MEDLINE=90005981; PubMed=2507354;
RA Onal T., Flitzgerald W.G., Atakawa S., Gocayne J.D., Urquhart D.A.,
RA Hall L.M., Fraser C.M., McCombie W.R., Venter J.C.;
RA "Cloning, sequence analysis and chromosome localization of a
RT drosophila muscarinic acetylcholine receptor.";
RL FEBS Lett. 255:219-225(1989).
-----
-1- FUNCTION: "THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
PI TURNOVER.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
CC
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DR EMBL; M27495; AAA85449.1; -
 DR EMBL; M23412; AAA28676.1; ALT_INIT.
 DR PIR; A36191; A36191.
 DR PIR; S05661; S05661.
 DR FlyBase; FBgn0000037; MACR-60C.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE; PS50262; G-PROTEIN_RECEP_FL_2; 1.
 DR Posttranslational; Multigene family: G-protein coupled receptor.
 KW phosphorylation; Multigene family: G-protein coupled receptor.

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 DOMAIN 50 60
 TRANSSEM 61 81
 DOMAIN 82 100
 TRANSSEM 101 120
 DOMAIN 121 140
 TRANSSEM 141 162
 DOMAIN 163 184
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 DOMAIN 5838 5858
 TRANSSEM 5859 5879
 DOMAIN 5880 5900
 TRANSSEM 5901 5921
 DOMAIN 5922 5942
 TRANSSEM 5943 5963
 DOMAIN 5964 5984
 TRANSSEM 5985 6005
 DOMAIN 6006 6026
 TRANSSEM 6027 6047
 DOMAIN 6048 6068
 TRANSSEM 6069 6089
 DOMAIN 6090 6110
 TRANSSEM 6111 6131
 DOMAIN 6132 6152
 TRANSSEM 6153 6173
 DOMAIN 6174 6194
 TRANSSEM 6195 6215
 DOMAIN 6216 6236
 TRANSSEM 6237 6257
 DOMAIN 6258 6278
 TRANSSEM 6279 6299
 DOMAIN 6300 6320
 TRANSSEM 6321 6341
 DOMAIN 6342 6362
 TRANSSEM 6363 6383
 DOMAIN 6384 6404
 TRANSSEM 6405 6425
 DOMAIN 6426 6446
 TRANSSEM 6447 6467
 DOMAIN 6468 6488
 TRANSSEM 6489 6509
 DOMAIN 6510 6530
 TRANSSEM 6531 6551
 DOMAIN 6552 6572
 TRANSSEM 6573 6593
 DOMAIN 6594 6614
 TRANSSEM 6615 6635
 DOMAIN 6636 6656
 TRANSSEM 6657 6677
 DOMAIN 6678 6698
 TRANSSEM 6699 6719
 DOMAIN 6720 6740
 TRANSSEM 6741 6761
 DOMAIN 6762 6782
 TRANSSEM 6783 6803
 DOMAIN 6804 6824
 TRANSSEM 6825 6845
 DOMAIN 6846 6866
 TRANSSEM 6867 6887
 DOMAIN 6888 6908
 TRANSSEM 6909 6929
 DOMAIN 6930 6950
 TRANSSEM 6951 6971
 DOMAIN 6972 6992
 TRANSSEM 6993 7012
 DOMAIN 7013 7033
 TRANSSEM 7034 7054
 DOMAIN 7055 7075
 TRANSSEM 7076 7096
 DOMAIN 7097 7117
 TRANSSEM 7118 7138
 DOMAIN 7139 7159
 TRANSSEM 7160 7180
 DOMAIN 7181 7201
 TRANSSEM 7202 7222
 DOMAIN 7223 7243
 TRANSSEM 7244 7264
 DOMAIN 7265 7285
 TRANSSEM 7286 7306
 DOMAIN 7307 7327
 TRANSSEM 7328 7348
 DOMAIN 7349 7369
 TRANSSEM 7370 7390
 DOMAIN 7391 7411
 TRANSSEM 7412 7432
 DOMAIN 7433 7453
 TRANSSEM 7454 7474
 DOMAIN 7475 7495
 TRANSSEM 7496 7516
 DOMAIN 7517 7537
 TRANSSEM 7538 7558
 DOMAIN 7559 7579
 TRANSSEM 7580 7600
 DOMAIN 7601 7621
 TRANSSEM 7622 7642
 DOMAIN 7643 7663
 TRANSSEM 7664 7684
 DOMAIN 7685 7705
 TRANSSEM 7706 7726
 DOMAIN 7727 7747
 TRANSSEM 7748 7768
 DOMAIN 7769 7789
 TRANSSEM 7790 7810
 DOMAIN 7811 7831
 TRANSSEM 7832 7852
 DOMAIN 7853 7873
 TRANSSEM 7874 7894
 DOMAIN 7895 7915
 TRANSSEM 7916 7936
 DOMAIN 7937 7957
 TRANSSEM 7958 7978
 DOMAIN 7979 7999
 TRANSSEM 8000 8020
 DOMAIN 8021 8041
 TRANSSEM 8042 8062
 DOMAIN 8063 8083
 TRANSSEM 8084 8104
 DOMAIN 8105 8125
 TRANSSEM 8126 8146
 DOMAIN 8147 8167
 TRANSSEM 8168 8188
 DOMAIN 8189 8209
 TRANSSEM 8210 8230
 DOMAIN 8231 8251
 TRANSSEM 8252 8272
 DOMAIN 8273 8293
 TRANSSEM 8294 8314
 DOMAIN 8315 8335
 TRANSSEM 8336 8356
 DOMAIN 8357 8377
 TRANSSEM 8378 8398
 DOMAIN 8399 8419
 TRANSSEM 8420 8440
 DOMAIN 8441 8461
 TRANSSEM 8462 8482
 DOMAIN 8483 8503
 TRANSSEM 8504 8524
 DOMAIN 8525 8545
 TRANSSEM 8546 8566
 DOMAIN 8567 8587
 TRANSSEM 8588 8608
 DOMAIN 8609 8629
 TRANSSEM 8630 8650
 DOMAIN 8651 8671
 TRANSSEM 8672 8692
 DOMAIN 8693 8713
 TRANSSEM 8714 8734
 DOMAIN 8735 8755
 TRANSSEM 8756 8776
 DOMAIN 8777 8797
 TRANSSEM 8798 8818
 DOMAIN 8819 8839
 TRANSSEM 8840 8860
 DOMAIN 8861 8881
 TRANSSEM 8882 8902
 DOMAIN 8903 8923
 TRANSSEM 8924 8944
 DOMAIN 8945 8965
 TRANSSEM 8966 8986
 DOMAIN 8987 9007
 TRANSSEM 9008 9028
 DOMAIN 9029 9049
 TRANSSEM 9050 9070
 DOMAIN 9071 9091
 TRANSSEM 9092 9112
 DOMAIN 9113 9133
 TRANSSEM 9134 9154
 DOMAIN 9155 9175
 TRANSSEM 9176 9196
 DOMAIN 9197 9217
 TRANSSEM 9218 9238
 DOMAIN 9239 9259
 TRANSSEM 9260 9280
 DOMAIN 9281 9301
 TRANSSEM 9302 9322
 DOMAIN 9323 9343
 TRANSSEM 9344 9364
 DOMAIN 9365 9385
 TRANSSEM 9386 9406
 DOMAIN 9407 9427
 TRANSSEM 9428 9448
 DOMAIN 9449 9469
 TRANSSEM 9470 9490
 DOMAIN 9491 9511
 TRANSSEM 9512 9532
 DOMAIN 9533 9553
 TRANSSEM 9554 9574
 DOMAIN 9575 9595
 TRANSSEM 9596 9616
 DOMAIN 9617 9637
 TRANSSEM 9638 9658
 DOMAIN 9659 9679
 TRANSSEM 9680 9700
 DOMAIN 9701 9721
 TRANSSEM 9722 9742
 DOMAIN 9743 9763
 TRANSSEM 9764 9784
 DOMAIN 9785 9805
 TRANSSEM 9806 9826
 DOMAIN 9827 9847
 TRANSSEM 9848 9868
 DOMAIN 9869 9889
 TRANSSEM 9890 9910
 DOMAIN 9911 9931
 TRANSSEM 9932 9952
 DOMAIN 9953 9973
 TRANSSEM 9974 9994
 DOMAIN 9995 10000

Query Match 49.4%; Score 40; DB 1; Length 722;
 Best Local Similarity 52.9%; Pred. No. 31;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 EKPPLTAAAPVYXNA 19
 DB 538 EDGEPTTAAAPLASAA 554

RESULT 7
 H2B_AGABI STANDARD; PRT; 143 AA.
 AC P78567;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Histone H2B.
 GN HTBA.
 OS Agaricus bisporus (Common mushroom).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Agaricaceae; Agaricus.

OX NCBI_TaxID=5341;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hors U1;
 RA MEDLINE=97111990; PubMed=8953726;
 RA Sonnenberg A.S.M., de Groot P.W.J., Schaap P.J., Baars J.J.P.,
 RA Visser J., van Griensven L.J.L.D.;
 RT "Isolation of expressed sequence tags of Agaricus bisporus and their
 RT assignment to chromosomes";
 RL Appl. Environ. Microbiol. 62:4542-4547(1996).
 CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
 CC H2A, H2B, H3, AND H4; WHICH WRAP APPROXIMATELY 146 BP OF DNA.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.

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DR EMBL; X94186; CA63898.1; -
 DR InterPro; IPR000558; Histone_H2B.
 DR InterPro; IPR004822; Histone_core.
 DR Pfam; PF00125; histone; 1.
 DR PRINTS; PR00621; HISTONEH2B.
 DR ProDom; PD000497; Histone_H2B; 1.
 DR SMART; SM00427; H2B; 1.
 DR PROSITE; PS00357; HISTONE_H2B; 1.
 DR Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
 KW Chromosomal protein; Nucleosome core; 6964010ZE31F456 CRC64;
 SQ SEQUENCE 143 AA; 15165 MW; 6964010ZE31F456 CRC64;

Query Match 48.1%; Score 39; DB 1; Length 143;
 Best Local Similarity 50.0%; Pred. No. 8.6;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 KTEPLTAAAPVYXNA 19
 DB 11 KAPASTAKAPVKSDA 26

RESULT 8
 DMPC_PSESP STANDARD; PRT; 486 AA.
 AC P19059;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE 2-hydroxymuconic semialdehyde dehydrogenase (EC 1.2.1.-) (HMSD).
 GN DMPC.
 OS Pseudomonas sp. (strain CF600).
 OG Plasmid pVil150.
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90304229; PubMed=2194577;
 RA Nordlund I., Shingler V.;
 RT "Nucleotide sequences of the meta-cleavage pathway enzymes 2-
 RT hydroxymuconic semialdehyde dehydrogenase and 2-hydroxymuconic
 RT semialdehyde hydrolase from Pseudomonas CF600";
 RL Biochim. Biophys. Acta 1049:227-230(1990).
 CC -1- FUNCTION: 2-HYDROXYMUCONIC ACID SEMIALDEHYDE CAN BE CONVERTED TO
 CC 2-HYDROXYMUTIC SEMIALDEHYDE EITHER DIRECTLY BY THE ACTION OF
 CC THREE SEQUENTIAL ENZYMES, THE FIRST OF WHICH IS HMSD.
 CC -1- PATHWAY: META-CLEAVAGE PATHWAY FOR THE DEGRADATION OF PHENOLS,
 CC CRESOLS AND CATECHOL. PHENOL METABOLISM.
 CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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EMBL: X52805: CAA36992.1: -

DR PIR: S10772: S10772.
DR HSSP: P20000: 1A68.
DR InterPro: IPR002086: Aldehyde_dehydr.
DR Pfam: PF00171: Aldehyde_1.
DR PROSITE: PS00070: ALDEHYDE_DEHYDR_GLU_1.
DR PROSITE: PS00687: ALDEHYDE_DEHYDR_GLU_1.
DR Aromatic hydrocarbons catabolism: Oxidoreductase; NAD; Plasmid.
KW ACT_SITE 254 254 BY SIMILARITY.
FT ACT_SITE 288 288 BY SIMILARITY.
SQ SEQUENCE 486 AA: 51682 MW: F906FCA64185AA68 CRC64:

Query Match 48.1%; Score 39; DB 1; Length 486;
Best Local Similarity 52.9%; Pred. No. 30;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy 3 EKTPLTTAAXAPVYXNA 19
Db 181 EETPLTTALLGEVQMA 197

RESULT 9
YB64_YEAST STANDARD; PRT; 527 AA.

AC P38314:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1994 (Rel. 36, Last annotation update)
DE Hypothetical 57.2 kDa protein in MEF2-HP2 intergenic region.
GN YBR314W OR YBR1501.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC NCBI_TaxID=4932;
OX (1)
RN SEQUENCE FROM N.A.
RP STRAIN=S288c;
RA Rieger M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE OF 114-527 FROM N.A.
RC STRAIN=S288c;
RA Dubois E., el Bakoury M., Glansdorff N., Messenguy F., Pierard A.,
RA Scherens B., Vierendeels F.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO YEAST YGL056C AND S.POMBE SDS23.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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CC EMBL: Z36083: CAA85178.1: -
CC PIR: S46088: S46088.
CC SGD: S0000418: SDS24.
CC InterPro: IPR000644: CBS_domain.
DR Pfam: PF00571: CBS; 4.
DR SMART: SM00116: CBS; 2.
KM Hypothetical protein: Repeat; CBS domain.
FT DOMAIN 196 251 CBS 1.
FT DOMAIN 283 335 CBS 2.
SQ SEQUENCE 527 AA: 57187 MW: DC2741550A69C154 CRC64:

Query Match 48.1%; Score 39; DB 1; Length 527;
Best Local Similarity 61.5%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 EKTPLTTAAXAP 14
Db 52 EETPLTTAAXAP 64

RESULT 10
VNUC_INBLE STANDARD; PRT; 560 AA.

AC P04665:
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE Nucleoprotein.
NP.
OS Influenza B virus (strain B/Lee/40).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus B.
OX NCBI_TaxID=11535;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=84174071; PubMed=6324462;
RA Briedis D.J., Tobin M.;
RT "Influenza B virus genome: complete nucleotide sequence of the
RT Influenza B/lee/40 virus genome RNA segment 5 encoding the
RT nucleoprotein and comparison with the B/Singapore/222/79
RT nucleoprotein."
RL Virology 133:448-455(1984).
CC -1- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.

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CC EMBL: K01395: AAA3689.1: -
DR InterPro: IPR002141: Flu_NP.
DR Pfam: PF00506: Flu_NP; 1.
KM Nucleoprotein.
SQ SEQUENCE 560 AA: 61770 MW: 74C4FEAF9E75A695 CRC64:

Query Match 48.1%; Score 39; DB 1; Length 560;
Best Local Similarity 44.4%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Oy 2 EKTPLTTAAXAPVYXNA 19
Db 19 EETPLTSGATRPITKPA 36

RESULT 11

GTRB_MYXXA STANDARD; PRT; 815 AA.

AC O33167:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA gyrase subunit B (EC 5.9.9.1.3).
GN GTRB.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision: Myxobacteria;
OC Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ER-15;

```

RA MEDLINE=98316655; PubMed=9654003;
RX Hayakawa Y., Noguchi H.,
RT "Growth-blocking peptide expressed in the insect nervous system:
RT cloning and functional characterization.";
RL Eur. J. Biochem. 253:810-816(1998).
RN [3]
RP STRUCTURE BY NMR OF 121-143.
RC TISSUE=Hemolymph;
RX MEDLINE=99107831; PubMed=9890941;
RA Aizawa T., Fujitani N., Hayakawa Y., Ohnishi A., Ohkubo T., Kumaki Y.,
RA Kawano K., Hikiuchi K., Nitta K.;
RT "Solution structure of an insect growth factor, growth-blocking
RT peptide.";
RL J. Biol. Chem. 274:1887-1890(1999).
CC -I- FUNCTION: BIOGENIC PEPTIDE THAT PREVENTS, IN LEPIDOPTERAN, THE
CC ONSET OF METAMORPHOSIS FROM LARVA TO PUPA. THIS GROWTH-BLOCKING
CC PEPTIDE HAS REPRESSIVE ACTIVITY AGAINST JUVENILE HORMONE ESTERASE.
CC -I- SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
CC -----
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CC -----
DR EMBL: S80564; AAB3742.1;
DR EMBL: AB012294; BA832793.1;
DR PDB: 1BQF; 09-DEC-98.
DR InterPro: IPR003463; GBP_PSP.
DR Pfam: PF02425; GBP_PSP; 1.
KW Hemolymph; signal; 3D-structure.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 120
FT PEPTIDE 121 143 GROWTH-BLOCKING PEPTIDE.
FT DISULFID 127 139
SQ SEQUENCE 143 AA; 15256 MW; DEBFBS27956840EB CRC64;

Query Match 46.9%; Score 38; DB 1; Length 143;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 10; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 2 EEXPT--LTTAXAPVNVNA 19
DB 83 DEVTPTTTTTHAAPTAVPNA 102
: ||| || || || ||
RESULT 13
PID_CORPS
ID PID_CORPS STANDARD; PRT; 307 AA.
AC P20626; Q59314;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Phospholipase D precursor (EC 3.1.4.4) (PID) (Choline phosphatase).
GN PID.
OS Corynebacterium pseudotuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=1719;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-47.
RX MEDLINE=90170833; PubMed=2407718;
RA Hodgson A.L.M., Bird P., Nisbet I.T.;
RT "Cloning, nucleotide sequence, and expression in Escherichia coli of
RT the phospholipase D gene from Corynebacterium pseudotuberculosis.";
RL J. Bacteriol. 172:1256-1261(1990).
RN [2]
RP SEQUENCE FROM N.A.

```

RA Songer J.G., Libby S.J., Tandolo J.J., Cuevas W.A.;
 RT "Cloning and expression of the phospholipase D gene from
 RL *Corynebacterium pseudotuberculosis* in *Escherichia coli*.";
 RN Infect. Immun. 58:131-136(1990).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Biovar equi / Isolate 155;
 RX MEDLINE-95255653; PubMed-7737503;
 RA McNamara P.J., Cuevas W.A., Songer J.G.;
 RT "Toxic phospholipases D of *Corynebacterium pseudotuberculosis*, C.
 RL *ulcerans* and *Arcanobacterium haemolyticum*: cloning and sequence
 RN homology.";
 RN Gene 156:113-118(1995).
 [4]
 RP MUTAGENESIS.
 RC STRAIN-Biovar ovls / Isolate Whetten 1;
 RX MEDLINE-95020614; PubMed-7934899;
 RA McNamara P.J., Bradley G.A., Songer J.G.;
 RT "Targeted mutagenesis of the phospholipase D gene results in
 RL decreased virulence of *Corynebacterium pseudotuberculosis*.";
 RN Mol. Microbiol. 12:921-930(1994).
 CC -1- FUNCTION: VIRULENCE FACTOR AFFECTING BACTERIAL DISSEMINATION AND
 CC SURVIVAL WITHIN THE HOST. HAS MAGNESIUM-DEPENDENT SPHINGOMELINASE
 CC AND HEMOLYTIC ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)O = choline + a
 CC phosphatidate.
 CC -1- SIMILARITY: TO OTHER *CORYNEBACTERIUM* PHOSPHOLIPASES D.
 CC -----
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 CC -----
 DR EMBL: L16587; AAA64910.1; -;
 DR EMBL: L16586; AAA99867.1; -;
 DR PIR: A35125; A35125.
 KW Hydrolyase; Lipid degradation; Magnesium; Virulence; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 307
 FT ACT_SITE 44 44
 FT VARIANT 5 6
 FT VARIANT 8 8
 FT VARIANT 189 189
 FT VARIANT 205 205
 FT VARIANT 270 270
 FT VARIANT 277 277
 SO SEQUENCE 307 AA; 33884 MW; D3B1334E6FC9875 CRC64;
 Query Match 46.9%; Score 38; DB 1; Length 307;
 Best Local Similarity 61.5%; Pred. No. 28;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 6 LTTAAAPVYN 18
 Db 18 PNCNMAAPVYN 30
 RESULT 14
 CATA_PSEPU STANDARD; PRT; 479 AA.
 ID CATA_PSEPU
 AC 059714;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Catalase (EC 1.11.1.6).
 GN CATA OR CATA.
 OS *Pseudomonas putida*.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 NCBI_TaxID=303;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Corvallis;
 RX MEDLINE-98019091; PubMed-9358059;
 RA Kim Y.C., Miller G.D., Anderson A.J.;
 RT "Identification of adjacent genes encoding the major catalase and a
 RL bacterioferritin from the plant-beneficial bacterium *Pseudomonas*
 RN *putida* 199:219-224(1997).
 CC -1- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN. SERVES
 CC TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) - O(2) + 2 H(2)O.
 CC -1- COFACTOR: HEME GROUP.
 CC -1- ENZYME REGULATION: ACTIVATED BY PEROXIDE.
 CC -1- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: U63511; AAB84219.1; -;
 DR HSSP; P42321; 2CAE.
 DR InterPro; IPR002226; Catalase.
 DR Pfam; PF00199; catalase: 1.
 DR PRINTS; PR00067; CATALASE.
 DR PRODOM; PD000510; Catalase.
 DR PROSITE; PS00437; CATALASE_1; 1.
 DR PROSITE; PS00438; CATALASE_2; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
 FT ACT_SITE 53 53
 FT ACT_SITE 126 126
 FT BINDING 336 336
 FT BINDING 336 336
 SO SEQUENCE 479 AA; 53381 MW; EF3CBDE6778571 CRC64;
 Query Match 46.9%; Score 38; DB 1; Length 479;
 Best Local Similarity 66.7%; Pred. No. 44;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 7 LTTAAAPVYN 18
 Db 5 LTTASGAPVDN 16
 RESULT 15
 EFG1_TREPA
 AC EFG1_TREPA
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE Elongation factor G 1 (EF-G 1).
 GN FUS4 OR FUS4-2 OR TP0767.
 OS *Treponema pallidum*.
 OC Bacteria; Spirochaetales; Spirochaetaceae; *Treponema*.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Nichols;
 RX MEDLINE-96332770; PubMed-9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.F., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Ullarback T.,
 RA McDonald L., Arlisch P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of *Treponema pallidum*, the syphilis
 RL spirochete.";
 Science 281:375-388(1998).

CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
 CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
 CC RIBOSOME.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC EF-G/EF-2 SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: AE001248; AAC65735.1; -.
 CC HSSP: P13551; 2EFG.
 CC TIGR: TP0767; -.
 DR InterPro: IPR004540; EF-G.
 DR InterPro: IPR000640; EFG_C.
 DR InterPro: IPR004161; EFTU_D2.
 DR InterPro: IPR000795; EF_GTPbind.
 DR InterPro: IPR005225; Small_GTP.
 DR Pfam: PF00009; GTP_EFTU; 1.
 DR Pfam: PF00679; EFG_G; 1.
 DR Pfam: PF03144; GTP_EFTU_D2; 1.
 DR PRINTS: PR00315; ELONGATNCT.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR TIGRFAMs: TIGR00484; EF-G; 1.
 DR PROSITE: PS00301; EFATOR_GTP; 1.
 DR Elongation factor: Protein biosynthesis; GTP-binding;
 DR Multigene family: Complete proteome.
 DR NP_BIND 15 22 GTP (BY SIMILARITY).
 DR NP_BIND 82 86 GTP (BY SIMILARITY).
 FT NP_BIND 136 139 GTP (BY SIMILARITY).
 SQ SEQUENCE 695 AA: 76831 MW: 46529898FE97E4E CRC64;

Query Match 46.98; Score 38; DB 1; Length 695;
 Best Local Similarity 60.08; Pred. No. 65;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 EEKTPITTAAXAPVY 16
 || | : | | | | |
 DB 295 EEPVTLSTDADAPVY 309

Search completed: March 14, 2003, 09:11:48
 Job time : 13 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:09:54 ; Search time 29 Seconds
(without alignments)
134.996 Million cell updates/sec

Title: US-09-359-426c-2

Sequence: 1 XEKPPLTTAAAPVXNA 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
|------------|-------|--------------|----------------|-----------------------|
| 1 | 48 | 59.3 | 480 16 08ZGS4 | 08ZGS4 Yersinia pe |
| 2 | 46 | 56.8 | 458 5 076672 | 076672 caenorhabdi |
| 3 | 45 | 56.6 | 484 2 09RG14 | 09RG14 actinobacti |
| 4 | 44 | 54.3 | 306 16 08XGWS | 08XGWS salmonella |
| 5 | 44 | 54.3 | 314 2 09A119 | 09A119 escherichia |
| 6 | 44 | 54.3 | 427 10 09AAQ0 | 09AAQ0 arabidopsis |
| 7 | 44 | 54.3 | 427 10 023188 | 023188 arabidopsis |
| 8 | 43 | 53.1 | 506 2 077924 | 077924 pseudomonas |
| 9 | 43 | 53.1 | 1240 12 09DMH8 | 09DMH8 rat cytochrome |
| 10 | 42 | 51.9 | 210 2 09RND2 | 09RND2 streptococ |
| 11 | 42 | 51.9 | 211 2 09XGWS | 09XGWS streptococ |
| 12 | 42 | 51.9 | 436 16 09FT45 | 09FT45 arabidopsis |
| 13 | 42 | 51.9 | 487 10 09RUK9 | 09RUK9 streptomyces |
| 14 | 41 | 50.6 | 132 2 09SE04 | 09SE04 oryza sativ |
| 15 | 41 | 50.6 | 417 2 054272 | 054272 streptomyces |
| 16 | 41 | 50.6 | 663 17 08ZGX0 | 08ZGX0 pyrobaculum |

| | | | | |
|----|------|------|---------------|----------------------|
| 17 | 41 | 50.6 | 1012 5 09V745 | 09V745 drosophila |
| 18 | 40 | 49.4 | 171 5 09U3E3 | 09U3E3 caenorhabdi |
| 19 | 40 | 49.4 | 212 5 09U4Y3 | 09U4Y3 ceratilis c |
| 20 | 40 | 49.4 | 232 17 09V984 | 09V984 betaproteum p |
| 21 | 40 | 49.4 | 258 16 08Y5M9 | 08Y5M9 listeria mo |
| 22 | 40 | 49.4 | 394 16 09A4B0 | 09A4B0 caulobacter |
| 23 | 40 | 49.4 | 477 16 09RD97 | 09RD97 streptomyces |
| 24 | 40 | 49.4 | 498 15 079665 | 079665 human immun |
| 25 | 40 | 49.4 | 554 5 09B1H5 | 09B1H5 halocynthia |
| 26 | 40 | 49.4 | 788 5 09M1B0 | 09M1B0 drosophila |
| 27 | 40 | 49.4 | 846 13 057577 | 057577 cynops pyr |
| 28 | 40 | 49.4 | 1360 5 002006 | 002006 drosophila |
| 29 | 40 | 49.4 | 1473 5 09VHP9 | 09VHP9 drosophila |
| 30 | 39.5 | 48.8 | 405 10 003462 | 003462 zea mays (m |
| 31 | 39.5 | 48.8 | 1793 5 09W596 | 09W596 drosophila |
| 32 | 39 | 48.1 | 235 10 09LGM5 | 09LGM5 oryza sativ |
| 33 | 39 | 48.1 | 395 11 091217 | 091217 mus musculu |
| 34 | 39 | 48.1 | 395 11 08R3V5 | 08R3V5 mus musculu |
| 35 | 39 | 48.1 | 410 2 09FD09 | 09FD09 streptococ |
| 36 | 39 | 48.1 | 419 16 08ZNG4 | 08ZNG4 human adeno |
| 37 | 39 | 48.1 | 484 12 09W4U2 | 09W4U2 human adeno |
| 38 | 39 | 48.1 | 484 16 09CPK5 | 09CPK5 pasteurella |
| 39 | 39 | 48.1 | 507 16 09ABX1 | 09ABX1 caulobacter |
| 40 | 39 | 48.1 | 518 13 09PTY0 | 09PTY0 cyprinus ca |
| 41 | 39 | 48.1 | 572 10 09LJG2 | 09LJG2 arabidopsis |
| 42 | 39 | 48.1 | 952 12 099174 | 099174 human adeno |
| 43 | 39 | 48.1 | 1353 5 018182 | 018182 caenorhabdi |
| 44 | 39 | 48.1 | 4900 5 09N541 | 09N541 caenorhabdi |
| 45 | 38.5 | 47.5 | 842 5 09VJH6 | 09VJH6 drosophila |

ALIGNMENTS

| RESULT 1 | ID | 08ZGS4 | PRELIMINARY: | PRT: | 480 AA. |
|----------|--|--------------------------------------|--------------|------|---------|
| AC | 08ZGS4 | 01-MAR-2002 (TREMBLrel. 20, Created) | | | |
| DT | 01-MAR-2002 (TREMBLrel. 20, Last sequence update) | | | | |
| DT | 01-JUN-2002 (TREMBLrel. 21, Last annotation update) | | | | |
| DE | Catalase (EC 1.11.1.6). | | | | |
| GN | KATA OR YPO1207. | | | | |
| OS | Yersinia pestis. | | | | |
| OC | Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; | | | | |
| OC | Yersinia. | | | | |
| OX | NCBI_TaxID=632. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=CO-92 / BIOVAR ORIENTALIS; | | | | |
| RX | MEDLINE=21470413; PubMed=11586360; | | | | |
| RA | Parkhill J., Wren B.W., Thomson N.R., Tiltball R.W., Holden M.T.G., | | | | |
| RA | Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L., | | | | |
| RA | Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M., | | | | |
| RA | Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., | | | | |
| RA | Feltwell T., Hamlin N., Holroyd S., Jagers K., Karlyshev A.V., | | | | |
| RA | Leather S., Mouton S., Oyston P.C.F., Quail M., Rutherford K., | | | | |
| RA | Stamonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; | | | | |
| RT | "genome sequence of Yersinia pestis, the causative agent of plague." | | | | |
| RL | Nature 413:523-527(2001). | | | | |
| DR | EMBL: A014147; CAC90045.1; " | | | | |
| DR | InterPro: IPR002226; Catalase. | | | | |
| DR | Pfam: PF00109; Catalase.1. | | | | |
| DR | ProDom: PD000510; Catalase.1. | | | | |
| DR | PROSITE: PS00438; CATALASE_2.1. | | | | |
| KW | Oxidoreductase; Peroxidase; Complete proteome. | | | | |
| SO | SEQUENCE 480 AA; 55023 MW; 27A72FBAF096347E CRC64; | | | | |

Query Match 59.3%; Score 48; DB 16; Length 480;
Best Local Similarity 68.8%; Pred. No. 8.6;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

| | |
|----------|---|
| CC | -i- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE (BY SIMILARITY). |
| CC | -i- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O. |
| DR | EMBL: AF162654; AAF17882.1; - |
| DR | HSSP: P42321.2CAG. |
| DR | InterPro: IPR002226; Catalase. |
| DR | Pfam: PF00199; catalase; 1. |
| DR | PRINTS: PR00067; CATALASE. |
| DR | ProDom: PD000510; Catalase; 1. |
| DR | PROSITE: PS00437; CATALASE_1; 1. |
| DR | PROSITE: PS00438; CATALASE_2; 1. |
| SW | Heme: Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase. |
| QY | SEQUENCE 484 AA; 54961 MW; D0E523AB257D8CB CRC64; |
| Db | Query Match 55.6%; Score 45; DB 2; Length 484; |
| | Best Local Similarity 83.3%; Pred. No. 27; |
| | Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0; |
| Qy | 7 LTTAAAPVYN 18 |
| | |
| Db | 14 LTTAAGAPVVDN 25 |
| RESULT 4 | |
| Q8XGW5 | PRELIMINARY; PRT; 306 AA. |
| ID | Q8XGW5 |
| AC | Q8XGW5; |
| DT | 01-MAR-2002 (TEMBLrel, 20, Created) |
| DT | 01-MAR-2002 (TEMBLrel, 20, Last sequence update) |
| DT | 01-JUN-2002 (TEMBLrel, 21, Last annotation update) |
| DE | Putative sugar kinase, ribokinase family (EC 2.7.1.15) (Putative |
| GN | carbohydrate kinase). |
| OS | STM3793 OR STY33989. |
| OS | Salmonella typhimurium, and |
| OC | Salmonella typhi. |
| OC | Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; |
| OC | Salmonella. |
| ON | NCBI_TaxID=602, 601; |
| RX | [1] |
| RP | SEQUENCE FROM N.A. |
| RC | SPECIES=S.typhimurium; STRAIN=LT2 / SGC1412 / ATCC 700720; |
| RX | MEDLINE=21534948; PubMed=11677609; |
| RA | McClelland M., Sanderson K.E., Speleth J., Clifton S.W., Latreille P., |
| RA | Courtney L., Porwollik S., Ali T., Dante M., Du F., Hou S., Layman D., |
| RA | Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulyaney E., |
| RA | Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M., |
| RA | Waterston R., Wilson R.K.; |
| RT | "Complete genome sequence of Salmonella enterica serovar Typhimurium |
| RL | LT2."; |
| RN | Nature 413:852-856(2001). |
| RN | [2] |
| RP | SEQUENCE FROM N.A. |
| RC | SPECIES=S.typhi; STRAIN=CT18; |
| RX | MEDLINE=21534947; PubMed=11677608; |
| RA | Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., |
| RA | Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M., |
| RA | Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., |
| RA | Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., |
| RA | Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., |
| RA | Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., |
| RA | Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., |
| RA | Whitehead S., Barrett B.G.; |
| RT | "Complete genome sequence of a multiple drug resistant Salmonella |
| RL | enterica serovar Typhi CT18."; |
| RL | Nature 413:848-852(2001). |
| DR | EMBL: AE008876; AA122651.1; - |
| DR | EMBL: AL627280; CAD03201.1; - |
| DR | InterPro: IPR002173; Pfkb. |
| DR | Pfam: PF00294; pfkb; 1. |
| KW | kinase; Transferase; Hypothetical protein; Complete proteome. |
| SEQUENCE | 306 AA; 33229 MW; 142A0289E2D1953 CRC64; |

Query Match 54.3% Score 44: DB 16: Length 306;
 Best Local Similarity 47.1% Pred. No. 25;
 Matches 8: Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 3 EKTPLTAAAXAPVXNA 19
 DB 84 EKVPCTSSGVAPIFVNA 100

RESULT 5
 ID 09A119 PRELIMINARY: PRT: 314 AA.
 AC 09A119:
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE Hypothetical 34.4 kDa protein.
 OS Escherichia coli.
 OC Bacteria: Proteobacteria: gamma subdivision: Enterobacteriaceae:
 NC Escherichia.
 NCBI_TaxID=562;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=AL862;
 RX MEDLINE=21101044; PubMed=11159989;
 RA Lallouf L., Le Bouguenec C.C.;
 RT "ata-8 Gene cluster is carried by a pathogenicity island inserted into
 the tRNA(Pro) of human and bovine pathogenic Escherichia coli
 isolates.";
 RL Infect. Immun. 69:937-948(2001).
 DR EMBL: AF286671; AAK7331.1;
 DR HSSP: P05054; 1RK2.
 DR InterPro: IPR002173; PfkB.
 DR InterPro: IPR002139; Ribokinase.
 DR Pfam: PF00294; PfkB; 1.
 DR PRINTS: PR00990; RIBOKINSE.
 DR Hypothetical protein.
 KW SEQUENCE 314 AA; 34415 MW; 2D5F7342C817E3B8 CRC64;
 SO

Query Match 54.3% Score 44: DB 2: Length 314;
 Best Local Similarity 47.1% Pred. No. 26;
 Matches 8: Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 3 EKTPLTAAAXAPVXNA 19
 DB 93 EKVPCTSSGVAPIFVNA 109

RESULT 6
 ID 094A00 PRELIMINARY: PRT: 427 AA.
 AC 094A00:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE Hypothetical 46.8 kDa protein.
 GN C7A10.390.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
 OC eurosids II: Brassicales; Brassicaceae; Arabidopsids.
 NC NCBI_TaxID=3702;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
 RA Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Tortum M.,
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
 RA Shun P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
 RA Ecker J.R., Theologis A.;
 RT "Full Length cDNA of gene C7A10.390 (GI:4006876).";

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF045887; AAK76561.1;
 KW Hypothetical protein.
 SO SEQUENCE 427 AA; 46788 MW; C8B0192D3150AE41 CRC64;

Query Match 54.3% Score 44: DB 10: Length 427;
 Best Local Similarity 60.0% Pred. No. 34;
 Matches 9: Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 EKTPLTAAAXAPV 16
 DB 208 EKAEMTTAMOSPV 222

RESULT 7
 ID 023188 PRELIMINARY: PRT: 427 AA.
 AC 023188:
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Hypothetical 46.8 kDa protein.
 GN C7A10.390 OR ATG636970.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
 OC eurosids II: Brassicales; Brassicaceae; Arabidopsids.
 NC NCBI_TaxID=3702;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Bavan M., Terry N., Vos P., Heljnen L., Mewes H.W., Schueller C.,
 RA Chalwatzis N.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project.
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z99707; CAB16794.1;
 DR EMBL: AL161590; CAB80363.1;
 KW Hypothetical protein.
 SO SEQUENCE 427 AA; 46800 MW; 75AC8E02D90AE54 CRC64;

Query Match 54.3% Score 44: DB 10: Length 427;
 Best Local Similarity 60.0% Pred. No. 34;
 Matches 9: Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 EKTPLTAAAXAPV 16
 DB 208 EKAEMTTAMOSPV 222

RESULT 8
 ID P77924 PRELIMINARY: PRT: 506 AA.
 AC P77924:
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Catalase isozyme.
 GN KAT4.
 OS Pseudomonas fluorescens.
 OC Plasmid PAM10.6.
 OC Bacteria: Proteobacteria: gamma subdivision: Pseudomonadaceae;
 OC Pseudomonas.
 NC NCBI_TaxID=294;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=CB36;
 RX MEDLINE=21318967; PubMed=11425481;
 RA Peters M., Helnar A., Nork A.;
 RT "Plasmid-encoded catalase KAT4, the main catalase of Pseudomonas
 fluorescens strain CB36.";
 RL FEMS Microbiol. Lett. 200:235-240(2001).;

DR EMBL: U72068; AAB17009.1; -
 DR HSP: P43321; 2CAE.
 DR InterPro: IPR002226; Catalase.
 DR Pfam: PF00199; catalase; 1.
 DR PRINTS: PR00067; CATALASE.
 DR PRODOM: PD000510; Catalase; 1.
 DR PROSITE: PS00438; CATALASE.2; 1.
 DR Plasmid.
 KW SEQUENCE 506 AA; 57324 MW; F1EAA728C5D41CBE CRC64;
 SQ
 Query Match
 Best Local Similarity 53.1%; Score 43; DB 2; Length 506;
 71.4%; Pred. No. 58;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 EKKPLTTAAXAPV 18
 DB 11 THLTTEGAPVVDN 24

RESULT 9
 Q9DWH8 PRELIMINARY; PRT: 1240 AA.
 AC Q9DWH8; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Pr2.
 GN R2.
 OS Rat cytomegalovirus (strain Maastricht).
 ON Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Murinegaleovirus.
 OX NCBI_Taxid=79700;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAASTRICHT;
 RX MEDLINE=2036325; Pubmed-10906222;
 RA Vink C., Beuken E., Bruggeman C.A.;
 RT "Complete DNA sequence of the rat cytomegalovirus genome";
 RL J. Virol. 74:7656-7665(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAASTRICHT;
 RX MEDLINE=20473137; Pubmed-11018281;
 RA Gruithuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
 RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
 RT spliced transcript";
 RL Virus Res. 69:119-130(2000).
 EMBL: AF232689; AAF9911.1; -
 SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;
 Query Match
 Best Local Similarity 53.1%; Score 43; DB 12; Length 1240;
 64.3%; Pred. No. 13e+02;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKKPLTTAAXAPV 15
 DB 570 EERRELTGASAPV 583

RESULT 10
 Q9RNU2 PRELIMINARY; PRT: 210 AA.
 AC Q9RNU2; 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Serum opacity factor precursor (Fragment).
 GN SOF4470.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_Taxid=1314;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=4470-96; TISSUE=Blood;
 RA Beall B., Gherardi G., Lovgren M., Tyrrell G., Packiam R., Forwick B.;
 RT "Predictions of M serotype, anti-opacity factor type, and highly
 RT related strain sets based upon the variable emm and sof gene
 RT sequences";
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF179217; AAD55775.1; -
 KW Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 7
 FT CHAIN 8 >210
 FT NON_TER 210 210
 SQ SEQUENCE 210 AA; 21220 MW; 199C89EBCF26086A CRC64;
 Query Match
 Best Local Similarity 51.9%; Score 42; DB 2; Length 210;
 57.1%; Pred. No. 38;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKPLTTAAXAPV 15
 DB 103 EKKPKVTWTSSTPV 116

RESULT 11
 Q9X6X8 PRELIMINARY; PRT: 211 AA.
 AC Q9X6X8; 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE Serum opacity factor precursor (Fragment).
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_Taxid=1314;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS1401 TYPE P1658;
 RA Beall B., Gherardi G.;
 RT "The relation of Streptococcus pyogenes sof and emm gene sequence
 RT types to genetically distinct strain sets";
 RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF154330; AAD36988.1; -
 KW Signal.
 FT NON_TER 1 1
 FT CHAIN <1 8
 FT NON_TER 9 >211
 FT NON_TER 211 211
 SQ SEQUENCE 211 AA; 21367 MW; F5475DDC6A084FE6 CRC64;
 Query Match
 Best Local Similarity 51.9%; Score 42; DB 2; Length 211;
 61.5%; Pred. No. 38;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKKPLTTAAXAPV 14
 DB 98 EKKPKVTWTSSTPV 110

RESULT 12
 Q9FT45 PRELIMINARY; PRT: 436 AA.
 AC Q9FT45; 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 17, Last annotation update)
 DE Hypothetical 48.1 kDa protein.
 GN T25B15_140.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;
 RN [1]
 RA SEQUENCE FROM N.A.
 RA Alcaraz J.P., Clebault G., Cottet A., Mache R., Mewes H.W., Rudd S.,
 RA Lemcke K., Mayer K.F.X., Quelet F., Salanoubat M.,
 RN Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RN Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL132972; CAC07928.1; -;
 DR InterPro: IPR000782; BgH3_fasciclin.
 DR InterPro: IPR000903; Nmt.
 DR Pfam: PF02469; Fasciclin_1.
 DR PROSITE: PS00976; NMT_2; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 436 AA; 48073 MW; 83FD94879F9855DF CRC64;
 Query Match 51.9%; Score 42; DB 10; Length 436;
 Best Local Similarity 50.0%; Pred. No. 74;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 OY 2 EKKPLTTAAXAPVYXNA 19
 DB 395 EKKTPVEKKTGVVYKKA 412

RESULT 13

ID O9RJK9 PRELIMINARY; PRT; 487 AA.
 AC O9RJK9;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Catalase (EC 1.11.1.6).
 GN KARA OR SC00379 OR SCF62.05.
 OS Streptomyces coelicolor.
 OC Bacteria: Filicutes: Actinobacteria: Actinobacteridae:
 OC Actinomycetales: Streptomycetales: Streptomycetaceae: Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Murphy L., Harris D.;
 RN Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RT [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
 RN Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Redenbach M., Kleser H.M., Denapalte D., Elchner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Collins M.,
 RA Harper D., Bateman A., Brown S., Chandra G., Hornsby T., Howarth M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth M.,
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";

RC Nature 417:141-147(2002).
 CC -1- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND
 CC SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
 CC PEROXIDE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) -> O(2) + 2 H(2)O.
 DR EMBL: AL121855; CAB58320.1; -;
 DR HSSP: P42321; 2CAE.
 DR InterPro: IPR002226; Catalase.
 DR Pfam: PF00199; catalase; 1.
 DR PRINTS: PR00067; CATALASE.
 DR PRODOM: PD000510; Catalase; 1.
 DR PROSITE: PS00437; CATALASE_1; 1.
 DR PROSITE: PS00438; CATALASE_2; 1.
 KW Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
 SQ SEQUENCE 487 AA; 55116 MW; 9D3334899EAF60B7 CRC64;
 Query Match 51.9%; Score 42; DB 16; Length 487;
 Best Local Similarity 69.2%; Pred. No. 82;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 6 PLTTAAXAPVYXN 18
 DB 8 PLTTVAGAPVPDN 20

RESULT 14

ID O9SE04 PRELIMINARY; PRT; 132 AA.
 AC O9SE04;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Copper chaperone homolog CCH.
 OS Oryza sativa (Rice).
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae;
 OC Eriarthroideae: Oryzoideae: Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98369102; PubMed=9701579;
 RA Himeblau E., Mira H., Lin S.-J., Culotta V.C., Penarrubia L.,
 RA Amasino R.M.;
 RT Identification of a functional homolog of the yeast copper
 RT homeostasis gene ATX1 from Arabidopsis.";
 RL Plant Physiol. 117:1227-1234(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Mira H., Penarrubia L.;
 RT "Copper chaperone from Oryza sativa.";
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF198626; AAF15285.1; -;
 DR HSSP: 000244; 1FE0.
 DR InterPro: IPR001934; Heavy_metal_transpt.
 DR Pfam: PF00403; HMA; 1.
 SQ SEQUENCE 132 AA; 13094 MW; 7176F95350A8231 CRC64;
 Query Match 50.6%; Score 41; DB 10; Length 132;
 Best Local Similarity 50.0%; Pred. No. 37;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 OY 2 EKKPLTTAAXAPVYXNA 19
 DB 97 ENAAPTAAEAFAIAAA 114
 RESULT 15
 ID O54272 PRELIMINARY; PRT; 417 AA.
 AC O54272;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

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DE Hypothetical aldehyde-dehydrogenase like 43.4 kDa protein
DS (EC 1.2.1.-).
OS Streptomyces hygroscopicus.
SC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_Taxid=1912;
|||
RN SEQUENCE FROM N.A..
RP STRAIN=SF1293;
RC MEDLINE=95309717; PubMed=7789803;
RX Hidaka T., Hidaka M., Kuzuyama T., Seto H.;
RA "Sequence of a P-methyltransferase-encoding gene isolated from a
RT biaphos-producing Streptomyces hygroscopicus.";
RL Gene 158:149-150(1995).
CC -I- PATHWAY: BIALAPHOS BIOSYNTHESIS.
CC -I- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
DR EMBL; D37877; BAN07116.1; -.
DR HSSP; P56533; 1A&S.
DR Interpro; IPR002086; Aldehyde-dehydr.
SR Pfam; PF00171; aldehyd; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
Hypothetical protein; Oxidoreductase.
FT ACT_SITE 187 BY SIMILARITY.
FT ACT_SITE 221 BY SIMILARITY.
SQ SEQUENCE 417 AA; 43406 MW; 9EB714F4FB654B47 CRC64;
Query Match 50.6%; Score 41; DB 2; Length 417;
Best Local Similarity 52.9%; Pred. No. 1e+02; Gaps 0;
Matches 9; Conservative 2; Mismatches 6; Indels 0;
QY 3 EKPTLTAAKAPVNVXNA 19
||||| |::|
DB 117 EKPTTALAFALLIRA 133

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